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OM protein - protein search, using sw model

Run on: November 19, 2004, 23:28:53 ; Search time 15.9718 Seconds
(without alignments)
202.141 Million cell updates/sec

Title: US-10-068-725-4_COPY_110_118
Perfect score: 48
Sequence: 1 SPVNLPPLE 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	57	AAU10953	Aau10953 Human AGP
2	48	100.0	166	AAW75785	Aaw75785 Human Lym
3	48	100.0	166	AAE15494	Aae15494 Human TAC
4	48	100.0	246	ABP97720	Abp97720 Amino aci
5	48	100.0	246	ADK00762	Adk00762 Native hu
6	48	100.0	247	AAI93398	Aay93398 Human BR4
7	48	100.0	247	ABR61797	Abx61797 Human RYZ
8	48	100.0	265	AAE09244	Aae09244 Human TAC
9	48	100.0	266	ABP97723	Abp97723 Amino aci
10	48	100.0	291	AAU10949	Aau10949 Human AGP
11	48	100.0	293	AAW75783	Aaw75783 Human Lym
12	48	100.0	293	AAE36312	Aab36312 Human neu
13	48	100.0	293	AAV94000	Aay94000 A transme
14	48	100.0	293	AAE09240	Aae09240 Human TAC
15	48	100.0	293	AAV71914	Aay71914 Human tra
16	48	100.0	293	AAO14130	Aao14130 Human tra
17	48	100.0	293	ABE88148	Abb88148 Human TAC
18	48	100.0	293	AAU99512	Aau99512 Human TAC
19	48	100.0	293	AAE28962	Aae28962 Human TAC
20	48	100.0	293	AAU75408	Aau75408 Tumour ne
21	48	100.0	293	AAU09900	Aau09900 Human AGP
22	48	100.0	293	AAE15493	Aae15493 Human tra
23	48	100.0	293	ABG71496	Abg71496 Human tum
24	48	100.0	293	AAE35211	Aae35211 Human TAC
25	48	100.0	293	ABP60551	Abp60551 Human tum

26	48	100.0	293	6	ABP97716	Abp97716 Amino aci
27	48	100.0	293	6	AAQ29592	Aao29592 Human DIT
28	48	100.0	293	7	ADF72628	Adf72628 Human tum
29	48	100.0	293	7	ADF77379	Adf77379 Human tum
30	48	100.0	293	8	ADK00754	Adk00754 Native hu
31	48	100.0	293	8	ADJ92514	Adj92514 Human TAC
32	48	100.0	293	8	ADN03174	Adn03174 Human TAC
33	48	100.0	294	8	ADK00765	Adk00765 hTACI spl
34	48	100.0	312	5	AAO14135	Aao14135 Protein o
35	48	100.0	357	6	AAE35226	Aae35226 Human TAC
36	48	100.0	392	6	AAE35223	Aae35223 Human TAC
37	48	100.0	397	5	AAE15498	Aae15498 Human TAC
38	48	100.0	404	5	AAO14136	Aao14136 Protein o
39	40	83.3	780	2	AAW11819	Aaw11819 Candida a
40	40	83.3	821	2	AAW16611	Aaw16611 Candida a
41	39	81.2	905	5	ABG93053	Abg93053 S. cerevi
42	39	81.2	905	6	ABR53130	Abx53130 Protein s
43	39	81.2	905	7	ADK62564	Adk62564 Disease t
44	38	79.2	84	4	AAU58271	Aau58271 Propionib
45	38	79.2	84	6	ABM54790	Abm54790 Propionib

ALIGNMENTS

RESULT 1

AAU10953
ID AAU10953 standard; protein; 57 AA.

XX AC AAU10953;

XX DT 12-MAR-2002 (first entry)

XX DE Human AGP-3 receptor stalk region.

XX KW Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;
KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;
KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;
KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;
KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;
KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
KW multiple sclerosis; Parkinson's disease; transgenic animal.

XX OS Homo sapiens.

XX PN WO200185782-A2.

XX PD 15-NOV-2001.

XX PF 12-FEB-2001; 2001WO-US004568.

XX PR 11-FEB-2000; 2000US-0181800P.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ, Hsu H;

XX WPI; 2002-049441/06.

XX PT Composition; useful for identifying modulator of receptor for treating
XX asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor
XX ligand family member) receptor and encoding nucleic acids.

XX PS Disclosure; Fig 18; 124pp; English.

XX CC The invention relates to a composition (I) comprising AGP-3 receptor
XX (tumour necrosis factor ligand family member) related protein (II)
XX attached to a vehicle protein. (I) is useful for modulating AGP-3-related
XX activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in
XX assays to identify cells and tissues that express AGP-3R or proteins

CC related to AGP-3R-related protein and for identifying compounds (agonists
 CC or antagonists) that interact with AGP-3R proteins. (II) is also useful
 CC for identifying intracellular proteins that interact with the respective
 CC cytoplasmic domains by yeast two-hybrid screening process. (II) is
 CC involved in B cell growth, survival and activation particularly in lymph
 CC node, spleen, and Peyer's patches. AGP-3R agonists and antagonists
 CC identified using (II) are used for modulating B cell response and are
 CC used to treat diseases characterised by inflammatory processes or
 CC deregulated immune response such as rheumatoid arthritis, graft-versus-
 CC host disease, Crohn's disease, lupus, etc. (II) is also useful in the
 CC production of hybridoma cells which are derived from B cells, which
 CC involves treating the hybridoma cells with (II). (II) is useful in the
 CC treatment of inflammatory conditions of joints, e.g., rheumatoid
 CC arthritis, osteoarthritis, etc. (II), its agonists or antagonists are
 CC useful for treating acute pancreatitis, ankyrothrophic lateral sclerosis
 CC (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia,
 CC diabetes, fever, glomerulonephritis, inflammatory bowel disease,
 CC ischaemic injury including cerebral ischaemia, multiple myeloma, multiple
 CC sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury,
 CC septic shock, etc. The nucleic acids are also useful for developing the
 CC transgenic animals expressing (II), which are useful for producing the
 CC polypeptides and for the study of in vivo biological activity. The
 CC present sequence represents the amino acid sequence of human AGP-3
 CC receptor stalk region #1
 XX SQ Sequence 57 AA;

Query Match 100.0%; Score 48; DB 5; Length 57;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
 DB 3 SPVNLPPPEL 11
 |||||

RESULT 2
 AAW75785
 ID AAW75785 standard; protein; 166 AA.

XX AC AAW75785;

XX DT 18-JAN-1999 (first entry)

XX DE Human lymphocyte surface receptor extracellular domain.

XX KW TAC1; transmembrane activator and CAML-interactor;
 XX KW calcium signal-modulating cyclophilin ligand; human;
 KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;
 KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;
 KW immunosuppressive; graft versus host disease; transplant rejection;
 KW therapy; signal transduction.

XX OS Homo sapiens.

XX FN WO9839361-A1.

XX PD 11-SEP-1998.

XX PF 03-MAR-1998; 98WO-US004270.

XX PR 03-MAR-1997; 97US-00810572.

XX PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX PI Bram RJ, Von Bulow G;

XX DR WPI: 1998-506346/43.

XX DR N-PSDB; AAV57330.

XX PT New isolated transmembrane activator protein - used to develop products
 XX for treating e.g. infections, cancers, autoimmune and inflammatory
 PT conditions, transplant rejection or graft-versus-host disease.

XX PS Claim 8; Page 73; 89pp; English.

XX CC This is the amino acid sequence of the N-terminal, i.e. the
 CC extracellular, domain of novel human transmembrane activator and CAML-
 CC interactor (TAC1) protein (see AAW75783). TAC1 is a lymphocyte receptor
 CC protein that is involved in the calcium activation pathway. It is
 CC normally present in B-lymphocytes, and to a much lesser extent in
 CC immature T-lymphocytes, and can therefore be targeted to specifically
 CC regulate B cell responses without affecting T cell activity. The
 CC extracellular domain of TAC1 functions as a binding site for a ligand
 CC that stimulates the activation of the cell by inducing the binding of the
 CC C-terminal portion (see AAW75784) of TAC1 to the N-terminal domain of
 CC CAML. A recombinant form of the extracellular portion of TAC1 acts as a
 CC dominant-negative or blocking agent and acts to suppress the immune
 CC system. It can be used to treat or prevent autoimmune disease, graft
 CC rejection or graft versus host disease. The extracellular region is also
 CC used in a claimed method for identifying a ligand for TAC1, in which
 CC binding of a candidate molecule is determined by detecting cellular
 CC activation of the AP-1, CAMP or NF-KB pathway, of NF-AT transcription
 CC factor, or of NF-AT dependent transcription
 XX SQ Sequence 166 AA;

Query Match 100.0%; Score 48; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
 DB 110 SPVNLPPPEL 118
 |||||

RESULT 3
 AAE15494
 ID AAE15494 standard; protein; 166 AA.

XX AC AAE15494;

XX DT 12-MAR-2002 (first entry)

XX DE Human TAC1 extracellular domain.

XX KW Human; transmembrane activator and intracellular CAML interactor; TAC1;
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 KW rheumatoid arthritis; atherosclerosis.

XX OS Homo sapiens.

XX FN WO200187979-A2.

XX PD 22-NOV-2001.

XX PF 14-MAY-2001; 2001WO-US015567.

XX PR 12-MAY-2000; 2000US-0204039P.

XX PR 27-JUN-2000; 2000US-0214591P.

XX PR 14-MAY-2001; 2001US-00214591.

XX PA (AMGE-) AMGEN INC.

XX PI Theill LE, Yu G;

XX DR WPI: 2002-066686/09.

XX PT Inhibiting activity of B cell maturation protein and/or transmembrane
 PT activator and intracellular cyclophilin ligand interactor, by
 PT administering a binding partner for APRIL, a tumor necrosis factor family

PT ligand.
 XX Claim 1; Fig 12A; 94pp; English.
 XX
 CC The invention relates to a method for inhibiting TAC1 (transmembrane
 CC activator and intracellular CAML interactor) and/or B cell maturation
 CC protein (BCMA) activity in a mammal. The method comprises administering a
 CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
 CC family ligand), having the consensus region of TAC1, BCMA, or the TAC1/
 CC BCMA extracellular consensus sequence, but not the extracellular region
 CC of TAC1 or BCMA. The method is useful for inhibiting activity of TAC1
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 CC lymphoproliferative disorders, one or more solid tumours such as lung,
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TAC1
 CC antagonists are useful for treating inflammation and immune function
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
 CC disease), drug and insect sting allergy, inflammatory bowel disease
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 CC with leucocyte infiltration of the skin or organs. The present sequence
 CC is human TAC1 protein extracellular domain
 XX
 SQ Sequence 166 AA;
 Query Match 100.0%; Score 48; DB 5; Length 166;
 Best Local Similarity 100.0%; Pred. No. 5.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPVNLPPPEL 9
 Db 110 SPVNLPPPEL 118
 |||||
 RESULT 4
 ABP97720
 ID ABP97720 standard; protein; 246 AA.
 AC ABP97720;
 XX
 DT 28-MAY-2003 (first entry)
 DE Amino acid sequence of human TAC1 receptor.
 XX
 KW Human; TAC1; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
 KW TALL-1; April; systemic lupus erythematosus.
 XX
 OS Homo sapiens.
 XX
 PN WO2003014294-A2.
 XX
 PD 20-FEB-2003.
 XX
 PF 24-JUL-2002; 2002WO-US023487.
 XX
 PR 03-AUG-2001; 2001US-0310114P.
 PR 30-APR-2002; 2002US-0377171P.
 XX
 XX (GETH) GENENTECH INC.
 PA
 PI Dixit V, Grewal I, Ridgway J, Yan M;
 XX
 DR WPI: 2003-256560/25.
 DR N-PSDB; ABZ68874.
 XX
 PT New nucleic acid encoding a TAC1s or BR3 polypeptide, useful for
 PT preparing a composition for treating systemic lupus erythematosus.
 XX
 PS Disclosure; Fig 5B; 153pp; English.
 XX
 CC The present sequence represents a human TAC1 polypeptide. The
 CC specification also describes BR3 polypeptides. TAC1 and BR3 are

CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
 CC bind to the TAC1 receptor, while TNF family ligands TALL-1 also binds to
 CC BR3 receptor. The TAC1 and BR3 receptor nucleic acid is useful for
 CC preparing a composition for treating systemic lupus erythematosus
 XX
 SQ Sequence 246 AA;
 Query Match 100.0%; Score 48; DB 6; Length 246;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SPVNLPPPEL 9
 Db 64 SPVNLPPPEL 72
 |||||
 RESULT 5
 ADK00762
 ID ADK00762 standard; protein; 246 AA.
 XX
 AC ADK00762;
 XX
 DT 06-MAY-2004 (first entry)
 DE Native human TAC1s.
 XX
 KW CAML interactor receptor; TAC1; Cytostatic; Antiinflammatory;
 KW Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic;
 KW Antidiabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;
 KW Antibacterial; antiparasitic; systemic lupus erythematosus;
 KW diabetes mellitus; AIDS.
 XX
 OS Homo sapiens.
 XX
 PN WO2004011611-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 25-JUL-2003; 2003WO-US023421.
 XX
 PR 25-JUL-2002; 2002US-0398530P.
 XX
 XX (GETH) GENENTECH INC.
 PA
 PI Chuntharapai A, Grewal I, Kim KJ, Yan M;
 XX
 DR WPI: 2004-143841/14.
 DR N-PSDB; ADK00761.
 XX
 PT New anti-TAC1 receptor monoclonal antibody, useful for diagnosing and
 PT treating pathological conditions associated with tumor necrosis factor,
 PT e.g. cancer or immune-related disease, such as rheumatoid arthritis or
 PT psoriasis.
 XX
 PS Disclosure; SEQ ID NO 14; 110pp; English.
 XX
 CC The present invention relates to an isolated monoclonal antibody which
 CC binds to a transmembrane activator of and CAML interactor (TAC1)
 CC receptor. The TAC1 antibodies are useful for modulating TALL-1 or TAC1
 CC polypeptide biological activity in mammalian cells, or for diagnosing and
 CC treating pathological conditions associated with TNF and TNF receptor-
 CC related molecules, e.g. cancer or immune-related disease, such as
 CC systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome,
 CC systemic vasculitis, diabetes mellitus, Crohn's disease,
 CC glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or
 CC infectious diseases including AIDS, hepatitis infection, bacterial
 CC infection, fungal infection, protozoal infection and parasitic infection.
 CC The present sequence represents native human TAC1s.
 XX
 SQ Sequence 246 AA;
 Query Match 100.0%; Score 48; DB 8; Length 246;
 Best Local Similarity 100.0%; Pred. No. 7.5;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
 Db 64 SPVNLPPPEL 72

RESULT 6
 ID AAY93998 standard; protein; 247 AA.
 XX AAY93998;
 AC AAY93998;
 DT 20-OCT-2000 (first entry)
 DE Human BR43x2, an isoform of the TACI receptor.
 XX Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Domain 1..120
 FT /note= "extracellular domain"
 FT Region 25..58
 FT /note= "cysteine-rich pseudo repeat"
 FT Domain 121..133
 FT /note= "transmembrane domain"
 FT Domain 134..247
 FT /note= "cytoplasmic domain"
 XX
 XX WO200040716-A2.
 XX
 XX 13-JUL-2000.
 XX
 XX 07-JAN-2000; 2000WO-US000396.
 XX
 XX 07-JAN-1999; 99US-00226533.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Gross JA, Xu W, Madden K, Yee DP;
 XX WPI; 2000-452538/39.
 XX N-PSDB; AAA58556.
 XX
 XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
 XX renal disease, graft versus host disease, and inflammation, comprises
 XX administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
 XX
 XX Claim 62; Page 145; 175pp; English.
 XX
 XX The present sequence represents a human BR43x2 polypeptide, which is an
 XX isoform of the transmembrane activator and CAML-interactor (TACI)
 XX receptor. TACI is a tumour necrosis factor (TNF) receptor. The
 XX extracellular domains of BR43x2, TACI or BCMA (a related B cell protein)
 XX contain a cysteine rich domain, and are used for inhibiting ztnf4
 XX activity. Ztnf4 is a TNF ligand. They may also be used for inhibiting
 XX BR43x2, TACI or BCMA receptor-ligand engagement associated with activated
 XX or resting B lymphocytes, effector T-cells or with antibody production.
 XX The antibody production is associated with an autoimmune disease selected
 XX from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis
 XX and rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA

CC receptor-ligand engagement is associated with asthma, bronchitis,
 CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,
 CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,
 CC light chain neuropathy, amyloidosis, moderating immune response,
 CC immunosuppression, graft rejection, Crohn's disease, joint
 CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
 CC pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA
 CC polypeptides, fusions, antibodies, agonists or antagonists can be used to
 CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol
 CC or renal emboli
 XX
 XX Sequence 247 AA;
 SQ

Query Match 100.0%; Score 48; DB 3; Length 247;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
 Db 64 SPVNLPPPEL 72

RESULT 7
 ABR61797
 ID ABR61797 standard; protein; 247 AA.
 XX ABR61797;
 AC ABR61797;
 XX
 DT 12-SEP-2003 (first entry)
 DE Human RYZN polypeptide.
 XX
 XX RYZN; TNFRSF; tumour necrosis factor receptor; antiarteriosclerotic;
 KW type III transmembrane protein; antidiabetic; hypotensive; antilipemic;
 KW human.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Domain 1..113
 FT /note= "extracellular domain"
 FT Domain 114..136
 FT /note= "transmembrane domain"
 FT Domain 137..247
 FT /note= "intracellular domain"
 XX
 XX WO2003045421-A1.
 XX
 XX 05-JUN-2003.
 XX
 XX 03-OCT-2002; 2002WO-IB004581.
 XX
 XX 28-NOV-2001; 2001US-0334152P.
 XX
 XX (GEST) GENSET SA.
 XX
 XX Dyalynas D, Scalia A, Lucas J, Briggs K;
 XX WPI; 2003-513616/48.
 XX N-PSDB; ACC84638.
 XX
 XX New agonists or antagonists of RYZN activity, useful for increasing or
 XX reducing body weight, for maintaining weight loss, and for preventing or
 XX treating an obesity-related disease or disorder, e.g. atherosclerosis or
 XX diabetes.
 XX
 XX Example; Page 32-33; 37pp; English.
 XX
 XX The invention relates to an agonist or antagonist of RYZN activity. RYZN
 XX is a member of the Tumour Necrosis Factor Receptor Super Family (TNFRSF)
 XX and is a type III transmembrane protein. The agonist or antagonist of
 XX RYZN activity, or compositions comprising them is useful for preventing
 XX or treating an obesity-related disease or disorder, such as insulin

CC resistance, hyperlipidemia, atherosclerosis, diabetes, hypertension, syndrome X, and hyperuricemia. These may also be used to increase or reduce body weight, or maintain weight loss. The present sequence represents the human RYZN polypeptide

XX SQ Sequence 247 AA;

Query Match 100.0%; Score 48; DB 7; Length 247;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
Db 64 SPVNLPPPEL 72
|||||

RESULT 8
AAE09244
ID AAE09244 standard; protein; 265 AA.

AC AAE09244;
DT 19-NOV-2001 (first entry)
XX

DE Human TAC1 splice variant protein.

XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
KW TAC1; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
XX

OS Homo sapiens.

XX WO200160397-A1.

XX 23-AUG-2001.

XX 28-NOV-2000; 2000WO-US032378.

XX 16-FEB-2000; 2000US-0182938P.

XX 22-AUG-2000; 2000US-0226986P.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
PI Yan M;

XX WPI; 2001-541628/60.

XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists.

XX Example 1; Fig 6; 160pp; English.

XX The invention relates to methods of using one or more agonists or
CC antagonists to modulate the activity of the members of TNF (tumour
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
CC TAC1 or BCMA. The method is useful for treating pathological conditions
CC or diseases associated with increased TALL-1 and APRIL expression or
CC activity. TALL-1 and APRIL antagonists are used to block the interaction
CC between APRIL and TALL-1 with TAC1 or BCMA. They are useful for treating
CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid
CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
CC present sequence is human TAC1 splice variant protein

XX Sequence 265 AA;

Query Match 100.0%; Score 48; DB 4; Length 265;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118
|||||

RESULT 9
ABP97723

ID ABP97723 standard; protein; 266 AA.

XX AC ABP97723;

XX 28-MAY-2003 (first entry)

XX Amino acid sequence of an alternatively spliced human TAC1 receptor.
XX Human; TAC1; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
KW TALL-1; April; systemic lupus erythematosus.

XX Homo sapiens.

XX WO2003014294-A2.

XX 20-FEB-2003.

XX 24-JUL-2002; 2002WO-US023487.

XX 03-AUG-2001; 2001US-0310114P.

XX 30-APR-2002; 2002US-0377171P.

XX (GETH) GENENTECH INC.

XX Dixit V, Grewal I, Ridgway J, Yan M;

XX WPI; 2003-256560/25.

XX New nucleic acid encoding a TAC1s or BR3 polypeptide, useful for
PT preparing a composition for treating systemic lupus erythematosus.

XX Disclosure; Fig 8; 153pp; English.

XX The present sequence represents an alternatively spliced human TAC1
CC polypeptide. The specification also describes BR3 polypeptides. TAC1 and
CC BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and
CC April bind to the TAC1 receptor, while TNF family ligands TALL-1 also
CC binds to BR3 receptor. The TAC1 and BR3 receptor nucleic acid is useful
CC for preparing a composition for treating systemic lupus erythematosus

XX Sequence 266 AA;

Query Match 100.0%; Score 48; DB 6; Length 266;

Best Local Similarity 100.0%; Pred. No. 8.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118
|||||

RESULT 10

AAU10949

ID AAU10949 standard; protein; 291 AA.

XX AC AAU10949;

XX 12-MAR-2002 (first entry)

XX Human AGP-3 receptor extracellular domain.

XX Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;
KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;
KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;
KW AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor;

mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder; rheumatoid arthritis; graft-versus-host disease; Crohn's disease; pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease; diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia; multiple sclerosis; Parkinson's disease; transgenic animal.

Homo sapiens.

W0200185782-A2.

15-NOV-2001.

12-FEB-2001; 2001WO-US004568.

11-FEB-2000; 2000US-0181800P.

(AMGE-) AMGEN INC.

Boyle WJ, Hsu H;

WPI; 2002-049441/06.

Composition, useful for identifying modulator of receptor for treating asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor ligand family member) receptor and encoding nucleic acids.

Claim 1; Fig 18; 12app; English.

The invention relates to a composition (I) comprising AGP-3 receptor (tumor necrosis factor ligand family member) related protein (II) attached to a vehicle protein. (I) is useful for modulating AGP-3-related activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in assays to identify cells and tissues that express AGP-3R or proteins related to AGP-3R-related protein and for identifying compounds (agonists or antagonists) that interact with AGP-3R proteins. (II) is also useful for identifying intracellular proteins that interact with the respective cytoplasmic domains by yeast two-hybrid screening process. (II) is involved in B cell growth, survival and activation particularly in lymph node, spleen, and Peyer's patches. AGP-3R agonists and antagonists identified using (II) are used for modulating B cell response and are used to treat diseases characterised by inflammatory processes or deregulated immune response such as rheumatoid arthritis, graft-versus-host disease, Crohn's disease, lupus, etc. (II) is also useful in the production of hybridoma cells which are derived from B cells, which involves treating the hybridoma cells with (II). (II) is useful in the treatment of inflammatory conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc. (II), its agonists or antagonists are useful for treating acute pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia, diabetes, fever, glomerulonephritis, inflammatory bowel disease, multiple ischaemic injury including cerebral ischaemia, multiple myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury, septic shock, etc. The nucleic acids are also useful for developing transgenic animals expressing (II), which are useful for producing the polypeptides and for the study of in vivo biological activity. The present sequence represents the amino acid sequence of human AGP-3 extracellular domain

Sequence 291 AA;

Query Match 100.0%; Score 48; DB 5; Length 291;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPEEL 9
| | | | |
Dd 110 SPVNLPEEL 118

RESULT 11
AAW75783
ID AAW75783 standard; protein; 293 AA.
XX

AC AAW75783;
XX 18-JAN-1999 (first entry)
XX Human lymphocyte surface receptor TACI.
DE
XX
XX
KW TACI; transmembrane activator and CAMU-interactor;
KW calcium signal-modulating cyclophilin ligand; human;
KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;
KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;
KW immunosuppressive; graft versus host disease; transplant rejection;
KW therapy.
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT Domain 1. .166
FT /label= Extracellular_domain
FT /note= "Claim 8"
FT Peptide 34. .71
FT /note= "TNFR_NGFR motif"
FT Domain 167. .186
FT /label= Transmembrane_domain
FT Domain 187. .294
FT /label= Cytoplasmic_domain
FT /note= "Claim 6"
XX
XX W098939361-A1.
PN
XX
XX 11-SEP-1998.
PD
XX
XX 03-MAR-1998; 98WO-US004270.
PF
XX
XX 03-MAR-1997; 97US-00810572.
PR
XX
XX (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
PA
XX
XX Bram RJ, Von Bulow G;
XX WPI; 1998-506346/43.
XX N-PSDB; AAV57328.
DR
XX
XX New isolated transmembrane activator protein - used to develop products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host disease.
PT
XX
XX Claim 20; Fig 2a; 89pp; English.
PS
XX
XX This is the amino acid sequence of novel human transmembrane activator and CAMU-interactor (TACI) protein, a lymphocyte receptor protein that is involved in the calcium activation pathway. TACI is normally present in B-lymphocytes, and to a much lesser extent in immature T-lymphocytes, and can therefore be targeted to specifically regulate B cell responses without affecting T cell activity. TACI cDNA (seeV57328) was isolated from a B-lymphocyte cDNA library using a yeast two-hybrid assay. Also claimed are the C-terminal (see AAW75784) and N-terminal (see AAW75785) fragments of TACI, recombinant DNA constructs, unicellular hosts, and antibodies to TACI protein. Methods are claimed for identifying a ligand for TACI and for identifying immunosuppressive drugs that selectively block the action of B lymphocytes without affecting mature T lymphocytes. TACI can be activated to increase immune system activity, e.g. for treating infections or cancers. It can be blocked to provide immunosuppression, e.g. for treating autoimmune and inflammatory conditions such as immune complex-induced vasculitis, glomerulonephritis, haemolytic anaemia, myasthenia gravis, type II collagen-induced arthritis, experimental allergic and hyperacute xenograft rejection, rheumatoid arthritis, systemic lupus erythematosus, transplant rejection, cancer or graft versus host disease
XX
XX Sequence 293 AA;

Query Match 100.0%; Score 48; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 9;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
 |||||
 Db 110 SPVNLPPPEL 118

RESULT 12

AAB36312
 ID AAB36312 standard; protein; 293 AA.

AC AAB36312;

DT 26-FEB-2001 (first entry)

XX Human neutrokin-alpha binding protein TR17 SEQ ID NO:2.

XX Human; neutrokin-alpha binding protein; NAR protein; TR17; cytostatic;
 KW immunosuppressive; neurotropic; neuroprotective; antiviral; antiallergic;
 KW hepatotropic; antidiabetic; antiinflammatory; antiulcer; cardiant;
 KW ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;
 KW autoimmune disorder.

XX Homo sapiens.

OS

XX WO200058362-A1.

PN

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AA94000;

20-OCT-2000 (first entry)

A transmembrane activator and CAML-interactor (TACI).

Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
 systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
 immune response; immunosuppression; graft rejection; joint pain;
 graft versus host disease; inflammation; swelling; anaemia; septic shock;
 insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 renal artery stenosis; occlusion; cholesterol; renal emboli.

XX Homo sapiens.

OS

XX WO200040716-A2.

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
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 Db 110 SPVNLPPPEL 118

RESULT 13

AAY94000
 ID AAY94000 standard; protein; 293 AA.

AC

DT

XX Human neutrokin-alpha binding protein TR17 SEQ ID NO:2.

XX Human; neutrokin-alpha binding protein; NAR protein; TR17; cytostatic;
 KW immunosuppressive; neurotropic; neuroprotective; antiviral; antiallergic;
 KW hepatotropic; antidiabetic; antiinflammatory; antiulcer; cardiant;
 KW ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;
 KW autoimmune disorder.

XX Homo sapiens.

OS

XX WO200058362-A1.

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
 |||||
 Db 110 SPVNLPPPEL 118

RESULT 12

AAB36312
 ID AAB36312 standard; protein; 293 AA.

AC AAB36312;

DT 26-FEB-2001 (first entry)

XX Human neutrokin-alpha binding protein TR17 SEQ ID NO:2.

XX Human; neutrokin-alpha binding protein; NAR protein; TR17; cytostatic;
 KW immunosuppressive; neurotropic; neuroprotective; antiviral; antiallergic;
 KW hepatotropic; antidiabetic; antiinflammatory; antiulcer; cardiant;
 KW ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;
 KW autoimmune disorder.

XX Homo sapiens.

OS

XX WO200058362-A1.

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
 |||||
 Db 110 SPVNLPPPEL 118

RESULT 13

AAY94000
 ID AAY94000 standard; protein; 293 AA.

AC

DT

XX Human neutrokin-alpha binding protein TR17 SEQ ID NO:2.

XX Human; neutrokin-alpha binding protein; NAR protein; TR17; cytostatic;
 KW immunosuppressive; neurotropic; neuroprotective; antiviral; antiallergic;
 KW hepatotropic; antidiabetic; antiinflammatory; antiulcer; cardiant;
 KW ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;
 KW autoimmune disorder.

XX Homo sapiens.

OS

XX WO200058362-A1.

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
 |||||
 Db 110 SPVNLPPPEL 118

RESULT 12

AAB36312
 ID AAB36312 standard; protein; 293 AA.

AC AAB36312;

DT 26-FEB-2001 (first entry)

XX Human neutrokin-alpha binding protein TR17 SEQ ID NO:2.

XX Human; neutrokin-alpha binding protein; NAR protein; TR17; cytostatic;
 KW immunosuppressive; neurotropic; neuroprotective; antiviral; antiallergic;
 KW hepatotropic; antidiabetic; antiinflammatory; antiulcer; cardiant;
 KW ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;
 KW autoimmune disorder.

XX Homo sapiens.

OS

XX WO200058362-A1.

PN

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RESULT 14
AAE09240
ID AAE09240 standard; protein; 293 AA.
XX AC
XX AAE09240;
XX
DT 19-NOV-2001 (first entry)
XX
XX Human TACI protein.
XX
XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
XX
OS Homo sapiens.
XX
PN WO200160397-A1.
XX
XX 23-AUG-2001.
XX
XX 28-NOV-2000; 2000WO-US032378.
XX
XX 16-FEB-2000; 2000US-0182938P.
XX
XX 22-AUG-2000; 2000US-0226986P.
XX
XX (GETH) GENENTECH INC.
XX
XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
PI Yan M;
PI
XX
XX WPI: 2001-541628/60.
XX
XX N-PSDB; AAD15901.
XX
XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
PT activity, for treating autoimmune disorders and cancer, comprises
PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
PT antagonists.
XX
XX Example 1; Fig 1; 160pp; English.
XX
XX The invention relates to methods of using one or more agonists or
CC antagonists to modulate the activity of the members of TNF (tumour
CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
CC TACI or BCMA. The method is useful for treating pathological conditions
CC or diseases associated with increased TALL-1 and APRIL expression or
CC activity. TALL-1 and APRIL antagonists are used to block the interaction
CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid
CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
CC present sequence is human TACI protein
XX
SQ Sequence 293 AA;
Query Match 100.0%; Score 48; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118
RESULT 15
AAY71914
ID AAY71914 standard; protein; 293 AA.
XX AC
XX AAY71914;
XX
DT 26-MAR-2001 (first entry)
XX

DE XX Human tumour necrosis factor receptor (TACI) protein.
KW Human; transmembrane activator and CAML interactor; TACI;
KW tumour necrosis factor receptor; TNF; autoimmune disease; diabetes;
KW calcium-signal modulating cyclophilin ligand; CAML; viral infection;
KW neutrokin alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy;
KW neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour;
KW antiarthritic; antirheumatic; immunosuppressive; multiple sclerosis;
KW rheumatoid arthritis; graft rejection; inflammation; cell proliferation;
KW cell death; immunoglobulin E-mediated allergic reaction; IgE.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 2. .166
FT /label= Extracellular domain
FT /note= "Binds with amino acids 123-285 of extracellular
FT domain of TACI-L"
XX
XX WO200067034-A1.
XX
XX 09-NOV-2000.
XX
XX 14-APR-2000; 2000WO-US010282.
XX
XX 30-APR-1999; 99US-00302863.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Goodwin RG, Din WS;
XX
XX WPI: 2001-016005/02.
XX
XX N-PSDB; AAD02006.
XX
XX Use of new interactions between tumor necrosis factor receptors (TACI)
PT and TACI ligands to screen candidate molecules for determining agonist
PT and antagonist interactions which are used for treating inflammation.
XX
XX Claim 10; Fig 1b; 46pp; English.
XX
XX The present sequence is a human tumour necrosis factor receptor (TACI)
CC protein. TACI (transmembrane activator and calcium-signal modulating
CC cyclophilin ligand (CAML)-interactor) forms a complex with neutrokin
CC alpha polypeptide (TACI-Ligand). The antagonist or agonist of TACI/TACI-L
CC complex is useful for modulating an intracellular signalling cascade
CC mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L complex are
CC used to inhibit the interaction between TACI and TACI-L for therapeutic
CC purposes to treat tumour and tumour metastasis and to combat various
CC autoimmune diseases e.g. multiple sclerosis and diabetes, as well as
CC other disorders, such as viral infection, rheumatoid arthritis, graft
CC rejection, and immunoglobulin (Ig) E-mediated allergic reactions and
CC inflammation. The interaction is used to study cellular processes
CC associated with tumour necrosis factor (TNF)-receptors such as immune
CC regulation, cell proliferation, cell death and inflammatory responses.
CC The interaction between the extracellular region of TACI and TACI-L can
CC be used to further develop understanding of which cell types TACI-L acts
CC upon
XX
SQ Sequence 293 AA;
Query Match 100.0%; Score 48; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118
Search completed: November 19, 2004, 23:40:03
Job time : 16.9718 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 23:37:09 ; Search time 7.09859 Seconds
(without alignments)
84.082 Million cell updates/sec

Title: US-10-068-725-4_COPY_110_118
Perfect score: 48
Sequence: 1 SPVNPPEL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/protdata/1/1aa/5A-COMB.pep.*
- 2: /cgn2_6/protdata/1/1aa/5B-COMB.pep.*
- 3: /cgn2_6/protdata/1/1aa/6A-COMB.pep.*
- 4: /cgn2_6/protdata/1/1aa/6B-COMB.pep.*
- 5: /cgn2_6/protdata/1/1aa/PCTUS-COMB.pep.*
- 6: /cgn2_6/protdata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	166	2	US-08-810-572A-6
2	48	100.0	166	3	US-09-290-333-6
3	48	100.0	166	4	US-09-782-857A-6
4	48	100.0	166	4	US-09-854-864-15
5	48	100.0	293	2	US-08-810-572A-2
6	48	100.0	293	3	US-09-290-333-2
7	48	100.0	293	4	US-09-782-857A-2
8	48	100.0	293	4	US-09-879-919-22
9	48	100.0	293	4	US-09-848-295-4
10	48	100.0	293	4	US-09-854-864-14
11	48	100.0	397	4	US-09-854-864-18
12	40	83.3	456	4	US-09-248-796A-19216
13	40	83.3	780	1	US-08-485-621-2
14	40	83.3	780	2	US-08-973-831-2
15	40	83.3	780	5	PCT-US96-09530A-2
16	38	79.2	458	4	US-09-252-991A-22614
17	37	77.1	1093	4	US-09-252-991A-21827
18	36	75.0	201	4	US-09-252-991A-32333
19	36	75.0	211	4	US-09-248-796A-22369
20	35	72.9	150	4	US-09-513-999C-6406
21	35	72.9	162	4	US-10-101-464A-526
22	35	72.9	642	4	US-09-252-991A-27045
23	35	72.9	1164	3	US-09-457-708-2
24	35	72.9	1164	4	US-09-950-046A-2
25	35	72.9	1164	4	US-09-976-594-989
26	34	70.8	268	3	US-08-652-877-4
27	34	70.8	268	3	US-08-476-515A-4

28	34	70.8	385	4	US-09-489-039A-11265	Sequence 11265, A
29	34	70.8	434	4	US-10-265-012-10	Sequence 10, Appl
30	34	70.8	569	4	US-10-265-012-8	Sequence 8, Appl
31	34	70.8	608	4	US-10-265-012-2	Sequence 2, Appl
32	34	70.8	943	3	US-08-476-515A-12	Sequence 12, Appl
33	34	70.8	944	3	US-08-652-877-12	Sequence 12, Appl
34	34	70.8	968	3	US-09-302-812-6	Sequence 6, Appl
35	34	70.8	968	3	US-09-511-477-6	Sequence 6, Appl
36	34	70.8	968	3	US-09-511-507-6	Sequence 6, Appl
37	34	70.8	4654	3	US-08-476-515A-84	Sequence 84, Appl
38	34	70.8	4655	3	US-08-652-877-84	Sequence 84, Appl
39	34	70.8	4655	3	US-08-652-877-86	Sequence 86, Appl
40	34	70.8	4655	3	US-08-652-877-88	Sequence 88, Appl
41	34	70.8	4655	3	US-08-652-877-90	Sequence 90, Appl
42	33	68.8	22	4	US-09-270-767-40902	Sequence 40902, A
43	33	68.8	22	4	US-09-270-767-56118	Sequence 56118, A
44	33	68.8	75	4	US-09-270-767-60082	Sequence 60082, A
45	33	68.8	148	4	US-09-270-767-39112	Sequence 39112, A

ALIGNMENTS

RESULT 1
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-810-572A-6

Query Match 100.0%; Score 48; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPEL 9
Db 110 SPVNLPEL 118

RESULT 2

US-09-290-333-6
; Sequence 6, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF

NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor

CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/290,333
FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:

ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-290-333-6

Query Match 100.0%; Score 48; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPEL 9
Db 110 SPVNLPEL 118

RESULT 3

US-09-782-857A-6
; Sequence 6, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz

TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS

CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor

CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/782,857A
FILING DATE: 14-Feb-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/810,572
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007

TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:

ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-857A-6

Query Match 100.0%; Score 48; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPEL 9
Db 110 SPVNLPEL 118

RESULT 4

US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent in version 3.1
SEQ ID NO 15
LENGTH: 166

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

Query Match 100.0%; Score 48; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.7; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

RESULT 5

US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-810-572A-2

Query Match 100.0%; Score 48; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

RESULT 6

US-09-290-333-2
; Sequence 2, Application US/09290333

; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2

Query Match 100.0%; Score 48; DB 3; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

RESULT 7

US-09-782-857A-2
; Sequence 2, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz

; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA


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;
;
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-857A-2

Query Match 100.0%; Score 48; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

RESULT 8
US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: P2253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293

Qy 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

Query Match 100.0%; Score 48; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

RESULT 9
US-09-848-295-4
; Sequence 4, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
; FILE REFERENCE: PF527
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-848-295-4

Query Match 100.0%; Score 48; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

RESULT 10
US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 14
US-09-854-864-14

Query Match 100.0%; Score 48; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118
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Db      110 SPVNLPEL 118
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US-09-854-864-18
; Sequence 18, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 18
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-18

Query Match      100.0%; Score 48; DB 4; Length 397;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SPVNLPEL 9
|||||
Db      110 SPVNLPEL 118

RESULT 12
US-09-248-796A-19216
; Sequence 19216, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19216
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (389)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-19216

Query Match      83.3%; Score 40; DB 4; Length 456;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PVNLPPE 8
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Db      255 PVNLPPE 261

RESULT 13
US-09-485-621-2
; Sequence 2, Application US/08485621
; Patent No. 5691187
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gerhold, David L.
; APPLICANT: Straus, Allyson Cole
; TITLE OF INVENTION: Anti-fungal Agents and Methods of
; TITLE OF INVENTION: Identifying and Using the Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSES: No. 5942386ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,621
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1584
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 780 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-621-2

Query Match      83.3%; Score 40; DB 1; Length 780;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 PVNLPPE 8
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Db      188 PVNLPPE 194

RESULT 14
US-08-973-831-2
; Sequence 2, Application US/08973831
; Patent No. 5942386
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gerhold, David L.
; APPLICANT: Straus, Allyson Cole
; TITLE OF INVENTION: Anti-fungal Agents and Methods of
; TITLE OF INVENTION: Identifying and Using the Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSES: No. 5942386ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,831
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,621
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1584
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 780 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-973-831-2

Query Match 83.3%; Score 40; DB 2; Length 780;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PVLNLPPE 8
Db 188 PVLNLPPE 194

RESULT 15

PCT-US96-09530A-2
Sequence 2, Application PC/TUS9609530A
GENERAL INFORMATION:
APPLICANT: Kmiec, Eric B.
APPLICANT: Gerhold, David L.
APPLICANT: Strauss, Allyson Cole
TITLE OF INVENTION: Anti-fungal Agents and Methods of
TITLE OF INVENTION: Identifying and Using the Same
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09530A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,621
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,399
FILING DATE: 21-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1970
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 780 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-09530A-2

Query Match 83.3%; Score 40; DB 5; Length 780;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PVLNLPPE 8
Db 188 PVLNLPPE 194

Search completed: November 19, 2004, 23:45:58
Job time : 11.0986 secs

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OM protein - protein search, using sw model

Run on: November 19, 2004, 23:40:10 ; Search time 24.4648 Seconds
(without alignments)
130.275 Million cell updates/sec

Title: US-10-068-725-4_COPY_110_118

Perfect score: 48
Sequence: 1 SPVNLPPPEL 9

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	48	100.0	166	9 US-09-854-864-15	Sequence 15, Appl
3	48	100.0	166	9 US-09-855-158-15	Sequence 15, Appl
4	48	100.0	166	14 US-10-293-816-6	Sequence 6, Appl
5	48	100.0	291	9 US-09-779-050A-43	Sequence 43, Appl
6	48	100.0	293	9 US-09-879-919-22	Sequence 22, Appl
7	48	100.0	293	9 US-09-854-864-14	Sequence 14, Appl
8	48	100.0	293	9 US-09-855-158-14	Sequence 14, Appl
9	48	100.0	293	9 US-09-961-376-2	Sequence 2, Appl
10	48	100.0	293	9 US-09-779-050A-42	Sequence 42, Appl
11	48	100.0	293	10 US-09-302-863-2	Sequence 2, Appl
12	48	100.0	293	10 US-09-855-564-2	Sequence 2, Appl
13	48	100.0	293	13 US-10-087-192-1650	Sequence 1650, Ap

14	48	100.0	293	13	US-10-084-971-2	Sequence 2, Appl
15	48	100.0	293	14	US-10-068-725-4	Sequence 4, Appl
16	48	100.0	293	14	US-10-151-882-46	Sequence 46, Appl
17	48	100.0	293	14	US-10-293-816-2	Sequence 2, Appl
18	48	100.0	293	14	US-10-008-063-8	Sequence 8, Appl
19	48	100.0	293	14	US-10-152-363A-2	Sequence 2, Appl
20	48	100.0	293	14	US-10-268-951-22	Sequence 22, Appl
21	48	100.0	293	15	US-10-258-368-1	Sequence 1, Appl
22	48	100.0	293	15	US-10-618-797-4	Sequence 4, Appl
23	48	100.0	293	17	US-10-743-634-7	Sequence 7, Appl
24	48	100.0	293	17	US-10-748-112-27	Sequence 27, Appl
25	48	100.0	301	15	US-10-258-368-12	Sequence 12, Appl
26	48	100.0	357	14	US-10-152-363A-56	Sequence 56, Appl
27	48	100.0	392	14	US-10-152-363A-50	Sequence 50, Appl
28	48	100.0	397	9	US-09-854-864-18	Sequence 18, Appl
29	48	100.0	397	9	US-09-855-158-18	Sequence 18, Appl
30	48	100.0	404	15	US-10-258-368-15	Sequence 15, Appl
31	43	89.6	538	17	US-10-425-115-271495	Sequence 271495,
32	40	83.3	519	17	US-10-425-115-221726	Sequence 221726,
33	39	81.2	452	15	US-10-424-599-216836	Sequence 216836,
34	39	81.2	905	16	US-10-451-457A-64	Sequence 64, Appl
35	39	81.2	1081	17	US-10-425-115-217364	Sequence 217364,
36	39	81.2	1304	17	US-10-425-115-217365	Sequence 217365,
37	39	81.2	1438	17	US-10-425-115-217355	Sequence 217355,
38	39	81.2	1540	17	US-10-425-115-217361	Sequence 217361,
39	39	81.2	1606	17	US-10-425-115-217360	Sequence 217360,
40	39	81.2	1742	17	US-10-425-115-254920	Sequence 254920,
41	39	81.2	1753	17	US-10-425-115-254923	Sequence 254923,
42	38	79.2	157	17	US-10-425-115-246652	Sequence 246652,
43	38	79.2	267	16	US-10-437-963-194387	Sequence 194387,
44	38	79.2	333	14	US-10-369-493-20124	Sequence 20124, A
45	38	79.2	346	14	US-10-369-493-18841	Sequence 18841, A

ALIGNMENTS

RESULT 1
US-09-779-050A-47
; Sequence 47, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-47

Query Match 100.0%; Score 48; DB 9; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
Db 3 SPVNLPPPEL 11

RESULT 2
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE

```
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.11
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

Query Match      100.0%; Score 48; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPVNLPEL 9
Db      110 SPVNLPEL 118

RESULT 3
US-09-855-158-15
; Sequence 15, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.11
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-15

Query Match      100.0%; Score 48; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPVNLPEL 9
Db      110 SPVNLPEL 118

RESULT 4
US-10-293-816-6
; Sequence 6, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
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; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-6

Query Match      100.0%; Score 48; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPVNLPEL 9
Db      110 SPVNLPEL 118

RESULT 5
US-09-779-050A-43
; Sequence 43, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-43

Query Match      100.0%; Score 48; DB 9; Length 291;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SPVNLPEL 9
Db      110 SPVNLPEL 118

RESULT 6
US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
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; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22

Query Match 100.0%; Score 48; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

RESULT 7

; Sequence 14, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BUYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-14

Query Match 100.0%; Score 48; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

RESULT 8

; Sequence 14, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-14

Query Match 100.0%; Score 48; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

RESULT 9

; Sequence 2, Application US/09961376
; Patent No. US20020106736A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
; FILE REFERENCE: PF524P1
; CURRENT APPLICATION NUMBER: US/09/961,376
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-376-2

Query Match 100.0%; Score 48; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
Db 110 SPVNLPPPEL 118

RESULT 10

; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

Query Match 100.0%; Score 48; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 17;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
| | | | | | | |
Db 110 SPVNLPPPEL 118

RESULT 11

US-09-302-863-2
; Sequence 2, Application US/09302863
; Publication No. US20030022233A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Wanwan S.
; TITLE OF INVENTION: METHODS OF USE OF THE TAC1/TAC1-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-09-302-863-2

Query Match 100.0%; Score 48; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
| | | | | | | |
Db 110 SPVNLPPPEL 118

RESULT 12

US-09-855-564-2
; Sequence 2, Application US/09855564
; Publication No. US20030165986A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Wanwan S.
; TITLE OF INVENTION: METHODS OF USE OF THE TAC1/TAC1-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/855,564
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/302,863
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-09-855-564-2

Query Match 100.0%; Score 48; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
| | | | | | | |
Db 110 SPVNLPPPEL 118

RESULT 13

US-10-087-192-1650
; Sequence 1650, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1650
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-1650

Query Match 100.0%; Score 48; DB 13; Length 293;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
| | | | | | | |
Db 110 SPVNLPPPEL 118

RESULT 14

US-10-084-971-2
; Sequence 2, Application US/10084971
; Publication No. US20020187526A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Neutrokin-alpha Binding Proteins and Methods Based Thereon
; FILE REFERENCE: PF524PCT
; CURRENT APPLICATION NUMBER: US/10/084,971
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/533,822
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-084-971-2

Query Match 100.0%; Score 48; DB 13; Length 293;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
| | | | | | | |
Db 110 SPVNLPPPEL 118

RESULT 15

US-10-068-725-4
; Sequence 4, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TAC1
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5


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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-4
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Query Match      100.0%; Score 48; DB 14; Length 293;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 SPVNLPPPEL 9
      |||||
Db      110 SPVNLPPPEL 118
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Job time : 24.4648 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 19, 2004, 23:34:49 ; Search time 3.29577 Seconds
(without alignments)
262.746 Million cell updates/sec

Title: US-10-068-725-4_COPY_110_118
Perfect score: 48
Sequence: 1 SPVNLPPPEL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	85.4	812	1 ISZPT1	DNA topoisomerase
2	41	85.4	814	2 T50327	dna topoisomerase
3	40	83.3	1011	2 T17430	tol protein - Neur
4	39	81.2	905	1 RBYSS	regulatory protein
5	38	79.2	277	2 I38857	microtubule-associ
6	38	79.2	384	2 AF2426	histidinol-phospha
7	38	79.2	2774	2 A43359	microtubule-associ
8	37	77.1	323	2 A93624	NADH dehydrogenase
9	37	77.1	323	2 A93622	NADH dehydrogenase
10	37	77.1	324	2 A90616	NADH dehydrogenase
11	37	77.1	324	2 T11167	NADH2 dehydrogenase
12	37	77.1	328	2 G9519	hypothetical prote
13	37	77.1	360	2 S72335	hypothetical prote
14	37	77.1	604	2 S58643	probable transcrip
15	37	77.1	1082	2 H81982	hypothetical prote
16	36	75.0	53	2 A61219	serpin Spi 1 - hor
17	36	75.0	54	2 S14338	serpin I - horse (
18	36	75.0	257	2 T40880	hypothetical prote
19	36	75.0	448	2 A70578	probable dap2 pro
20	36	75.0	467	2 B87070	probable peptidase
21	36	75.0	514	2 A36793	hypothetical prote
22	36	75.0	563	2 T44214	probable phosphor
23	36	75.0	563	2 T44029	Ganciclovir kinase
24	36	75.0	656	2 AF1040	Vi polysaccharide
25	36	75.0	656	2 A56975	Vi polysaccharide
26	36	75.0	947	2 I49635	mouse Dhml protein
27	36	75.0	962	2 S58107	hypothetical WD-40
28	36	75.0	1188	2 S49915	extensin-like prot
29	36	75.0	1706	2 B75633	probable RNA helic

30	36	75.0	1791	2 T02909	hypothetical prote
31	36	75.0	1939	2 AF0095	probable sideropho
32	35	72.9	51	2 B61219	serpin Spi 2 - hor
33	35	72.9	172	2 T21753	hypothetical prote
34	35	72.9	295	2 C87599	conserved hypothet
35	35	72.9	345	2 G75202	dipeptide abc tran
36	35	72.9	477	2 G83048	probable two-compo
37	35	72.9	711	1 S28391	protein-tyrosine-p
38	35	72.9	711	2 T45160	protein-tyrosine-p
39	35	72.9	744	2 T20969	hypothetical prote
40	35	72.9	823	2 B83905	hypothetical prote
41	35	72.9	1012	2 I53172	RAE-28 - mouse
42	35	72.9	1161	2 H95903	probable chemotaxi
43	35	72.9	1164	2 T03814	tumor suppressor p
44	34	70.8	110	2 C64598	hypothetical prote
45	34	70.8	229	2 T51587	filamentous flower

ALIGNMENTS

RESULT 1

ISZPT1

DNA topoisomerase (EC 5.99.1.2) - fission yeast (Schizosaccharomyces pombe)
N:Alternate names: nicking-closing enzyme; omega-protein; relaxing enzyme; swivelase; ty
C:Species: Schizosaccharomyces pombe
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: S03329
R:Uemura, T.; Morino, K.; Uzawa, S.; Shiozaki, K.; Yanagida, M.
Nucleic Acids Res. 15, 9727-9739, 1987
A:Title: Cloning and sequencing of Schizosaccharomyces pombe DNA topoisomerase I gene,
A:Reference number: S03329; MUID:88096534; PMID:2827111
A:Accession: S03329
A:Molecule type: DNA
A:Residues: 1-812 <UEMS>
A:Cross-references: UNIPROT:P07799; EMBL:X06201; NID:G5118; PIDN:CAA29559.1; PID:G5119
C:Comment: Type I DNA topoisomerase catalyzes the ATP-independent transient breakage of
in another, followed by rejoining. This reaction will lead to the conversion of one to
C:Genetics: 5/1; 36/3
A:Introns: 5/1; 36/3
C:Superfamily: eukaryotic type I DNA topoisomerase
C:Keywords: DNA binding; DNA replication; heterotetramer; isomerase
F:771/Active site: Tyr #status Predicted

Query Match

Best Local Similarity 85.4%; Score 41; DB 1; Length 812;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPE 8

Db 221 NPVNLPPPE 228

RESULT 2

T50327

dna topoisomerase I [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
R:McDougall, R.C.; Rajadream, M.A.; Barrell, B.G.; Cadieu, E.; Lelaure, V.; Galibert, F.
submitted to the EMBL Data Library, January 2000
A:Reference number: Z25061
A:Accession: T50327
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-814 <MCD>
A:Cross-references: UNIPROT:P07799; EMBL:AL136536; PIDN:CA566458.1; GSPDB:GNO0067; SPDB

QY 1 SPVNLPPPE 8

Db 221 NPVNLPPPE 228

Query Match 85.4%; Score 41; DB 2; Length 814;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPE 8
:|||||
Db 223 NPVNLPE 230

RESULT 3
T17430
tol protein - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R;Shiu, P.K.; Glass, N.L.
Genetics 151, 545-555, 1999
A;Title: Molecular characterization of tol, a mediator of mating-type associated vegetative incompatibility
A;Reference number: Z18781; MUID:99126425; PMID:9927450
A;Accession: T17430
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1011 <SH1>
A;Cross-references: UNIPROT:O93882; EMBL:AF085183; NID:g3777586; PID:g3777587; PIDN:AA06
C;Genetics:
A;Gene: tol
A;Introns: 266/1
C;Function:
C;Superfamily: Neurospora crassa tol protein

Query Match 83.3%; Score 40; DB 2; Length 1011;
Best Local Similarity 86.7%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPVNLPE 9
:|||||
Db 85 SPINIPHL 93

RESULT 4
RBY55
regulatory protein SNF5 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YBR2036; protein YBR289w
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1991 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
A;Accession: S44551; S46171; A36375; S12067; S39145
R;Holmstrom, K.; Brandt, T.; Kalliesoe, T.
Yeast 10 (Suppl. A), S47-S62, 1994
A;Title: The sequence of a 32430 bp segment located on the right arm of chromosome II fr
A;Reference number: S44537; MUID:94378722; PMID:8091861
A;Accession: S44551
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-905 <HOL>
A;Cross-references: UNIPROT:P19480; EMBL:X76053; NID:g600025; PIDN:CAA53652.1; PID:g4291
R;Brandt, T.; Christensen, C.; Holmstrom, K.; Kalliesoe, T.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S46157
A;Accession: S46171
A;Molecule type: DNA
A;Residues: 1-905 <BRA>
A;Cross-references: EMBL:Z36158; NID:g536741; PIDN:CAA85254.1; PID:g536742; GSPDB:GN0000
R;Laurent, B.C.; Treitel, M.A.; Carlson, M.
Mol. Cell. Biol. 10, 5616-5625, 1990
A;Title: The SNF5 protein of Saccharomyces cerevisiae is a glutamine- and proline-rich b
A;Reference number: A36375; MUID:91042489; PMID:2233708
A;Accession: A36375
A;Molecule type: DNA
A;Residues: 1-563, 'D', 565-905 <LAU>
A;Cross-references: GB:M36482; NID:g172637; PIDN:AAA35062.1; PID:g172638
C;Genetics:

A;Gene: SGD:SNF5; MIPS:YBR289w
A;Cross-references: SGD:S0000493; MIPS:YBR289w
A;Map position: 2R
C;Superfamily: regulatory protein SNF5
C;Keywords: nucleus; transcription regulation
F;31-324/Region: glutamine/proline-rich
F;435-683/Region: acidic
F;714-882/Region: proline-rich

Query Match 81.2%; Score 39; DB 1; Length 905;
Best Local Similarity 55.6%; Pred. No. 65;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPEL 9
:|||||
Db 120 APINLPPI 128

RESULT 5
I38857
microtubule-associated protein 1A - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: I38857
R;Fukuyama, R.; Rapoport, S.I.
J. Neurosci. Res. 40, 820-825, 1995
A;Title: Brain-specific expression of human microtubule-associated protein 1A (MAP1A) ge
A;Reference number: I38857; MUID:95356255; PMID:7629894
A;Accession: I38857
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-277 <RES>
A;Cross-references: UNIPROT:P78559; EMBL:U14577; NID:g642451; PIDN:AAA81362.1; PID:g64245
C;Genetics:
A;Gene: GDB:MAP1A
A;Cross-references: GDB:I32858; OMIM:600178
A;Map position: 15q13-15qter
C;Superfamily: microtubule-associated protein MAP1B

Query Match 79.2%; Score 38; DB 2; Length 277;
Best Local Similarity 87.5%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPVNLPE 8
:|||||
Db 170 SPVGLPE 177

RESULT 6
AF2426
histidinol-phosphate aminotransferase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AF2426
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, S.
Nakazaki N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF2426
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-384 <KUR>
A;Cross-references: UNIPROT:QBYMG7; GB:BA000019; PIDN:BAB76665.1; PID:g17134104; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: hisC
C;Superfamily: histidinol-phosphate aminotransferase

Query Match 79.2%; Score 38; DB 2; Length 384;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 9

A99622

NADH dehydrogenase chain 1 NDI [imported] - Anomalopteryx didiformis mitochondrion

C/Species: mitochondrion Anomalopteryx didiformis

C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004

C/Accession: A99622

R/Haddrath, O.; Baker, A.J.

Proc. R. Soc. Lond. B Biol. Sci. 268, 939-945, 2001

A/Title: Complete mitochondrial DNA genome sequences of extinct birds: ratite phylogen

A/Reference number: A99613; MUID:21263106; PMID:11370967

A/Accession: A99622

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-323 <KUR>

A/Cross-references: UNIPROT:Q957V7; GB:NC_002779; NID:G14141926; PIDN:NP_115363.1; GSPDB

C/Genetics:

A/Gene: NDI

A/Genome: mitochondrion

A/Genetic code: SGC1

C/Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t

C/Keywords: mitochondrion

Query Match 77.1%; Score 37; DB 2; Length 323;

Best Local Similarity 77.8%; Pred. No. 47;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9

| : |||||

Db 252 SSLNLPPPEL 260

RESULT 10

A90616

NADH dehydrogenase chain 1 NDI [imported] - Pterocnemia pennata mitochondrion

C/Species: mitochondrion Pterocnemia pennata

C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004

C/Accession: A90616

R/Haddrath, O.; Baker, A.J.

Proc. R. Soc. Lond. B Biol. Sci. 268, 939-945, 2001

A/Title: Complete mitochondrial DNA genome sequences of extinct birds: ratite phylogene

A/Reference number: A99613; MUID:21263106; PMID:11370967

A/Accession: A90616

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-324 <KUR>

A/Cross-references: UNIPROT:Q95888; GB:NC_002783; NID:G14141898; PIDN:NP_115415.1; GSPDB

C/Genetics:

A/Gene: NDI

A/Genome: mitochondrion

A/Genetic code: SGC1

C/Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-t

C/Keywords: mitochondrion

Query Match 77.1%; Score 37; DB 2; Length 324;

Best Local Similarity 77.8%; Pred. No. 47;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9

| : |||||

Db 252 SSLNLPPPEL 260

RESULT 11

T11167

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - greater rhea mitochondrion

C/Species: mitochondrion Rhea americana (greater rhea, common rhea)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C/Accession: T11167; T11416

R/Mindell, D.P.; Sorenson, M.D.; Dimcheff, D.E.

Proc. Natl. Acad. Sci. U.S.A. 95, 10693-10697, 1998

A/Title: Multiple independent origins of mitochondrial gene order in birds.

A;Accession: T11167
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-324 <MIN>
 A;Cross-references: UNIPROT:O79392; EMBL:AF090339; NID:g4894475; PID:g4894476; PIDN:AA03
 R;Harlid, A.
 Submitted to the EMBL Data Library, May 1999
 A;Reference number: Z17270
 A;Accession: T11416
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-284, 'P', 286-324 <HAR>
 A;Cross-references: EMBL:Y16884; PIDN:CAA76501.2
 C;Genetics:
 A;Genome: mitochondrion
 A;Genetic code: SGC1
 C;Superfamily: NADH:quinone oxidoreductase (complex I), subunit 1/[NiFe]-hydrogenase-3-b
 C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
 Query Match 77.1%; Score 37; DB 2; Length 324;
 Best Local Similarity 77.8%; Pred. No. 47;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 SPVNLPPPEL 9
 | : |||||
 Db 252 SSLNLPPPEL 260
 RESULT 12
 G96519
 hypothetical protein T2J15.14 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: G96519
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Matti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: G96519
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-328 <STO>
 A;Cross-references: UNIPROT:Q9C7Y7; GB:AE005173; NID:gi0645466; PIDN:AAG21580.1; GSPDB:G
 C;Genetics:
 A;Gene: T2J15.14
 A;Map position: 1

Query Match 77.1%; Score 37; DB 2; Length 328;
 Best Local Similarity 66.7%; Pred. No. 48;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
 | : |||||
 Db 106 SPLNLPPPEL 114

RESULT 13

G72235
 hypothetical protein - Thermotoga maritima (strain MSB8)
 C;Species: Thermotoga maritima
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: G72235
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Steward, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A;Reference number: A72200; MUID:99287316; PMID:10360571
 A;Accession: G72235
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-360 <ARN>
 A;Cross-references: UNIPROT:Q9X1R9; GB:AE001803; GB:AE000512; NID:g4982150; PIDN:AA036650
 A;Experimental source: strain MSB8
 C;Genetics:
 A;Gene: TMI583
 C;Superfamily: Thermotoga maritima hypothetical protein TMI583

Query Match 77.1%; Score 37; DB 2; Length 360;
 Best Local Similarity 75.0%; Pred. No. 53;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PVNLPPPEL 9
 | : |||||
 Db 171 PVSIPPEL 178

RESULT 14

S58643
 probable transcription factor SPT20 - yeast (Saccharomyces cerevisiae)
 N;Alternate names: protein AOE555; protein O0452; protein YOL148c
 C;Species: Saccharomyces cerevisiae
 C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S58643; S60388; S66845; S57676
 R;Roberts, S.M.; Winston, F.
 Submitted to the EMBL Data Library, March 1995
 A;Reference number: S58643
 A;Accession: S58643
 A;Molecule type: DNA
 A;Residues: 1-604 <ROB>
 A;Cross-references: UNIPROT:P50875; EMBL:U22063; NID:g722280; PID:g722281
 R;Casamayor, A.; Aldea, M.; Casas, C.; Herrero, E.; Gamo, F.J.; Lafuente, M.J.; Gancedo,
 Yeast 11, 1281-1288, 1995
 A;Title: DNA sequence analysis of a 13 kbp fragment of the left arm of yeast chromosome 1
 A;Reference number: S60385; MUID:96132030; PMID:8553699
 A;Accession: S60388
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 50-292, 'S', 294-604 <CAS>
 A;Cross-references: EMBL:248239; NID:gl163073; PIDN:CAA88279.1; PID:g886948
 R;Arino, J.; Casamayor, A.; Gamo, F.J.; Gancedo, C.; Lafuente, M.J.; Aldea, M.; Casas, C.
 Submitted to the Protein Sequence Database, July 1996
 A;Reference number: S66814
 A;Accession: S66845
 A;Molecule type: DNA
 A;Residues: 1-604 <ARI>
 A;Cross-references: EMBL:Z74890; NID:gi420051; PID:e252310; PID:gi420052; MIPS:YOL148C
 A;Experimental source: strain S288C
 C;Genetics:
 A;Gene: SGD:SPT20; ADA5
 A;Cross-references: SGD:S0005508; MIPS:YOL148C
 A;Map position: 15L

Query Match 77.1%; Score 37; DB 2; Length 604;
 Best Local Similarity 66.7%; Pred. No. 94;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
 | : |||||
 Db 30 SPVNVPPPM 38

RESULT 15

H81982
 hypothetical protein NMA0631 [imported] - Neisseria meningitidis (strain Z2491 serogroup
 C;Species: Neisseria meningitidis
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C;Accession: H81982
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel]

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A:Reference number: A81775; MUID:20222556; PMID:10761919
A:Accession: H81982
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1082 <PAR>
A:Cross-references: UNIPROT:Q9JYX9; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB8392
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA0631
C:Superfamily: *Neisseria meningitidis* hypothetical protein NMA0631

Query Match 77.1%; Score 37; DB 2; Length 1082;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
||:|||||
DB 370 SPLNLSPEL 378

Search completed: November 19, 2004, 23:44:58
Job time : 8.29577 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 23:32:13 ; Search time 32.1972 Seconds
(without alignments)
160.833 Million cell updates/sec

Title: US-10-068-725-4_COPY_110_118
Perfect score: 48
Sequence: 1 SPVNLPPPEL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02:*

1: uniprot_sprot:*

2: uniprot_treml:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	247	Q726F5	Q726F5 homo sapien
2	48	100.0	293	T13X_HUMAN	O14836 homo sapien
3	41	85.4	814	TOPI_SCHPO	P07799 schizosacch
4	41	85.4	1289	Q7RKÅ2	Q7RKÅ2 plasmodium
5	40	83.3	778	TOPI_CANAL	Q00313 candida alb
6	40	83.3	1011	Q93882	Q93882 neurospora
7	40	83.3	1044	Q6M9G4	Q6M9G4 neurospora
8	40	83.3	1044	CAF05993	Q6Q228 uncultured
9	39	81.2	62	Q6Q228	Q6Q228 uncultured
10	39	81.2	62	AAS90616	AAS90616 unculture
11	39	81.2	292	Q82X60	Q82X60 nitrosomona
12	39	81.2	330	Q89QS3	Q89QS3 bradyrhizob.
13	39	81.2	854	Q9FVG6	Q9FVG6 zea mays (m
14	39	81.2	905	SNF5_YEAST	P18480 saccharomyc
15	39	81.2	1124	Q9CM76	Q9CM76 pascheurella
16	38	79.2	261	Q7U5L2	Q7U5L2 synchococc
17	38	79.2	276	Q7QXT8	Q7QXT8 giardia lam
18	38	79.2	381	Q7VTR0	Q7VTR0 bordetella
19	38	79.2	381	Q7W2A3	Q7W2A3 bordetella
20	38	79.2	381	Q7WR70	Q7WR70 bordetella
21	38	79.2	384	H182_ANASP	Q8YMG7 anabaena sp
22	38	79.2	389	Q725T0	Q725T0 desulfovibr
23	38	79.2	389	AAS97813	AAS97813 desulfovi
24	38	79.2	447	Q8RPM1	Q8RPM1 ehrlichia c
25	38	79.2	536	Q89VW5	Q89VW5 bradyrhizob
26	38	79.2	563	Q8BI72	Q8BI72 mus musculus
27	38	79.2	564	Q7XA49	Q7XA49 glycine max
28	38	79.2	579	Q8TBM5	Q8TBM5 homo sapien
29	38	79.2	580	Q9NXXV6	Q9NXXV6 homo sapien
30	38	79.2	581	Q7V7K8	Q7V7K8 prochloroco
31	38	79.2	631	Q9NYH0	Q9NYH0 homo sapien

32	38	79.2	703	2	Q9ST08	Q9st08 brassica ca
33	38	79.2	751	2	Q888J6	Q888j6 pseudomonas
34	38	79.2	992	2	Q8L499	Q8l499 oryza sativ
35	38	79.2	1085	2	Q755J0	Q755j0 ashbya gosa
36	38	79.2	1085	2	AAS53207	Aas53207 ashbya go
37	38	79.2	1089	2	Q9FN97	Q9fn97 arabidopsia
38	38	79.2	1153	2	Q8S0G6	Q8s0g6 oryza sativ
39	38	79.2	2774	1	MAPA_RAT	P34926 ratus norv
40	38	79.2	2805	1	MAPA_HUMAN	P78559 homo sapien
41	37	77.1	68	2	Q7OUU3	Q7ouu3 ochotona pr
42	37	77.1	68	2	CAD60951	Cad60951 ochotona
43	37	77.1	299	2	Q7NEJ4	Q7nej4 gloobacter
44	37	77.1	323	2	Q9B6X0	Q9b6x0 dinornis gi
45	37	77.1	323	2	Q9B6Z3	Q9b6z3 casuaris b

ALIGNMENTS

RESULT 1

Q7Z6F5 PRELIMINARY; PRT; 247 AA.
AC Q7Z6F5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane activator and CAML interactor.
GN Name=TNFRSF13B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY302137; AAP57629.1; -;
KW GO; GO:0016021; C:integral to membrane; IEA.
KW Transmembrane.
SQ SEQUENCE 247 AA; 26664 MW; 850E1F4C257858E6 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
Db |||||
64 SPVNLPPPEL 72

RESULT 2

T13X_HUMAN STANDARD; PRT; 293 AA.
ID T13X_HUMAN
AC O14836;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).
GN Name=TNFRSF13B; Synonym=TACI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA von Buelow G.-U., Bram R.J.;
RL MEDLINE=97458245; PubMed=9311921;
RT "NF-AT activation induced by a CAML-interacting member of the tumor necrosis factor receptor superfamily.";
RL Science 278:138-141(1997).
RN [2]

SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heleth F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP FUNCTION.
RX MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200;
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D.,
RA Migone T.S., Nardelli B., Wei P., Ruben S.M., Ulrich S.J.,
RA Olsen H.S., Kanakara P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RT high affinity receptor for TNF family members APRIL and BlyS.";
RL J. Biol. Chem. 275:35478-35485(2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
RN [5]
RP INTERACTIONS WITH TRAF2 AND TRAF5.
RX MEDLINE=20341628; PubMed=10880535;
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,
RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
RA Meng S.Y., Boyle W.J., Hsu H.;
RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT factor family member involved in B cell regulation.";
RL J. Exp. Med. 192:137-143(2000).
CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity.
CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAML2 with its C-terminus.
CC -1- SUBCELLULAR LOCATION: Type III membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
CC intestine and peripheral blood leukocytes. Expressed in resting B-
CC cells and activated T-cells, but not in resting T-cells.
CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
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CC -----
DR EMBL; AF023614; AAC51790.1; -;
DR EMBL; BC028072; AAH28072.1; -;
DR HSPG; Q9Y275; IQDD.
DR Genew; HGNC:18153; TNFRSF13B.
DR MIM; 604907; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR InterPro; IPR001368; TNFR C6.
DR PROSITE; PS00652; TNFR NGFR 1; 1.
DR PROSITE; PS00652; TNFR NGFR 2; FALSE NEG.
KW Glycoprotein; Immune response; Receptor; Repeat; Signal-anchor;
KW Transmembrane.
FT DOMAIN 1 165 Extracellular (Potential).
FT DOMAIN 166 186 Signal-anchor for type III membrane
FT DOMAIN 187 293 protein (Potential).
FT REPEAT 33 67 Cytoplasmic (Potential).
FT REPEAT 70 104 TNFR-Cys 1.
FT REPEAT 104 128 TNFR-Cys 2.
FT DISULFID 34 47 By similarity.
FT DISULFID 50 62 By similarity.
FT DISULFID 54 66 By similarity.
FT DISULFID 71 86 By similarity.
FT DISULFID 89 100 By similarity.
FT DISULFID 93 104 By similarity.
FT CARBOHYD 128 128 N-linked (GlcNAc..) (Potential).
FT CONFLICT 251 251 P -> L (in Ref. 2).
SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;
Query Match 100.0%; Score 48; DB 1; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SPVNLPEEL 9
DB 110 SPVNLPEEL 118

RESULT 3
TOP1 SCHPO STANDARD; PRT; 814 AA.
AC P07759; Q9P7V7;
DT 01-AUG-1988 (Rel. 08, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE DNA topoisomerase I (EC 5.99.1.2).
GN Name=TopI; ORFNames=SPC1703.14c;
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
RN NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=88096534; PubMed=2827111;
RA Uemura T., Morino K., Uzawa S., Shiozaki K., Yanagida M.;
RT "Cloning and sequencing of Schizosaccharomycetes pombe DNA topoisomerase
RT I gene, and effect of gene disruption.";
RL Nucleic Acids Res. 15:9727-9739(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Rucke E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor K.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritz C., Holzer C., Moestl D., Hilbert H.,
Borrmann K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Galibert F., Vesey S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Armstrong J., Revuelta J.B., Moreno S., Armstrong J., Forsburg S.B.,
Derutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
"The genome sequence of *Schizosaccharomyces pombe*.";
Nature 415:871-880(2002).
[3]
[3]
ACTIVE SITE TYROSINE.
MEDLINE=8934041; PubMed=2547758;
Eng W.-K., Pandit S.D., Sternglanz R.;
"Mapping of the active site tyrosine of eukaryotic DNA topoisomerase
I".
J. Biol. Chem. 264:13373-13376(1989).
CC -1- FUNCTION: The reaction catalyzed by topoisomerases leads to the
conversion of one topological isomer of DNA to another.
CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
DNA, followed by passage and rejoining.
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
negative and positive supercoils, whereas prokaryotic enzymes
relax only negative supercoils.
CC -1- MISCELLANEOUS: When a topoisomerase transiently breaks a DNA
backbone bond, it simultaneously forms a protein-DNA link, in
which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus
at one end of the enzyme-severed DNA strand.
CC -1- SIMILARITY: Belongs to the eukaryotic type I topoisomerase family.

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ENBL; X6201; CAA39559.1; --
ENBL; AU136536; CAB66458.1; --
PIR; S03329; ISZPT1.
PIR; T50327; T50327.
HSP; P04786; 1O1S.
GENEB Spombe; SPBC1703.14C; --
InterPro; IPR011010; DNA_brk_join_enz.
InterPro; IPR001631; Topisemrse_I.
InterPro; IPR009054; Topisemrse_insert.
InterPro; IPR008336; Topoisomer_I_N.
Pfam; PF01028; Topoisom_I_1.
Pfam; PF02919; Topoisom_I_N; 1.
PRINTS; PR00416; EUTPISMRASE1.
SMART; SM00435; TOPEUC; 1.
DR PROSITE; PS00176; TOPOISOMERASE_I_EUK; 1.
KW DNA-binding; Isomerase; Topoisomerase.
FT ACT SITE 773 773 DNA cleavage.
FT CONFLICT 7 8 Missing (in Ref. 1).
FT CONFLICT 308 308 Q -> E (in Ref. 1).
FT CONFLICT 446 446 S -> N (in Ref. 1).
FT CONFLICT 698 698 V -> M (in Ref. 1).
SQ SEQUENCE 814 AA; 93980 MW; 842D8D81C92C80A3 CRC64;

Query Match 85.4%; Score 41; DB 1; Length 814;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RN SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10321 / CCM 8215;
 RX MEDLINE=96242310; PubMed=9026437;
 RA Taylor A., Giles K., Sarthy A.V., McConigal T., Postel J.;
 RT "Identification of the gene encoding DNA topoisomerase I from *Candida albicans*.";
 RL FEMS Microbiol. Lett. 138:113-121 (1996).
 RP
 RX SEQUENCE FROM N.A.
 RM MEDLINE=97195784; PubMed=90431115;
 RA Jiang W., Gerhold D., Knice E.B., Hauser M., Becker J.M., Koltin Y.;
 RT "The topoisomerase I gene from *Candida albicans*.";
 RL Microbiology 143:377-386 (1997).
 CC
 CC -1- FUNCTION: The reaction catalyzed by topoisomerases leads to the
 CC conversion of one topological isomer of DNA to another.
 CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
 CC DNA, followed by passage and rejoining.
 CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
 CC negative and positive supercoils, whereas prokaryotic enzymes
 CC relax only negative supercoils.
 CC -1- MISCELLANEOUS: When a topoisomerase transiently breaks a DNA
 CC backbone bond, it simultaneously forms a protein-DNA link, in
 CC which a tyrosyl oxygen in the enzyme is joined to a DNA phosphorus
 CC at one end of the enzyme-severed DNA strand.
 CC -1- SIMILARITY: Belongs to the eukaryotic type I topoisomerase family.
 CC
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 CC EMBL; U40454; AAC49381.1; -.
 CC EMBL; U41342; AAB39507.1; -.
 CC HSP; P04786; 1015.
 CC InterPro; IPR011010; DNA_brk_join_enz.
 CC InterPro; IPR001631; Topoisomerase I.
 CC InterPro; IPR008336; Topoisomerase I_N.
 CC Pfam; PF01028; Topoisom I; 1.
 CC Pfam; PF02919; Topoisom I; 1.
 CC PRINTS; PR00416; EUTPISMRASEI.
 CC SMART; SM00435; TOPEUC; 1.
 CC PROSITE; PS00176; TOPOISOMERASE_I_EUK; 1.
 KW DNA-binding; Isomerase; Topoisomerase.
 FT ACT_SITE 736 736
 FT CONFLICT 2 2 N -> S (in Ref. 2).
 FT CONFLICT 61 61 K -> KRK (in Ref. 2).
 FT CONFLICT 465 465 L -> F (in Ref. 2).
 FT CONFLICT 623 623 I -> L (in Ref. 2).
 FT CONFLICT 710 710 R -> K (in Ref. 2).
 SQ SEQUENCE 778 AA; 90484 MW; BFABR6B22EA2E5D3 CRC64;

 Query Match 83.3%; Score 40; DB 1; Length 778;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 PVNLPPE 8
 DB 186 PVNLPPE 192

 RESULT 6
 O93882 PRELIMINARY; PRT; 1011 AA.
 AC O93882
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE TOL.
 GN Name=tol;
 OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99126425; PubMed=9927450;
 RA Shiu P.K.T., Glass N.L.;
 RT "Molecular characterization of tol, a mediator of mating-type-
 RT associated vegetative incompatibility in *Neurospora crassa*.";
 RL Genetics 151:545-555 (1999).
 DR EMBL; AF085183; AAC64945.1; -.
 DR PIR; T17430; T17430.
 DR InterPro; IPR010730; HET.
 DR Pfam; PF06985; HET; 1.
 SQ SEQUENCE 1011 AA; 113718 MW; EC1B7C5187F73FE7 CRC64;

 Query Match 83.3%; Score 40; DB 2; Length 1011;
 Best Local Similarity 66.7%; Pred. No. 3.1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 1 SPVNLPPPEL 9
 DB 85 SPINIPPHL 93

 RESULT 7
 Q6M9G4 PRELIMINARY; PRT; 1044 AA.
 AC Q6M9G4
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Protein TOL.
 GN Name=G21B4.080;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX908808; CAF05993.1; -.
 DR InterPro; IPR010730; HET.
 DR Pfam; PF06985; HET; 1.
 SQ SEQUENCE 1044 AA; 117616 MW; EB1DCE2AFC41F287 CRC64;

 Query Match 83.3%; Score 40; DB 2; Length 1044;
 Best Local Similarity 66.7%; Pred. No. 3.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 1 SPVNLPPPEL 9
 DB 85 SPINIPPHL 93

 RESULT 8
 CAF05993 PRELIMINARY; PRT; 1044 AA.
 ID CAF05993
 AC CAF05993
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Protein TOL.
 GN G21B4.080.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte V., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX90808; CAF05993.1; -;
 SQ SEQUENCE 1044 AA; 117616 MW; EB1DCE2AFC41F287 CRC64;

Query Match 83.3%; Score 40; DB 2; Length 1044;
 Best Local Similarity 66.7%; Pred. No. 3.2e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
 ||:|||||
 DB 85 SPINIPPHL 93

RESULT 9

Q6Q228 PRELIMINARY; PRT; 62 AA.
 ID Q6Q228;
 AC Q6Q228;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative glucosamine-fructose-6-phosphate aminotransferase
 DE (Fragment).
 OS uncultured soil bacterium.
 OC Bacteria; environmental samples.
 OX NCBI_TaxID=164851;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Riesenfeld C.S., Goodman R.M., Handelsman J.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY566824; AAS90616.1; -;
 DR GO; GO:0008483; F:transaminase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Amino transferase; Transferase.
 FT NON_TER 1
 SQ SEQUENCE 62 AA; 6835 MW; 4BFCBC9E94F35A4E CRC64;

Query Match 81.2%; Score 39; DB 2; Length 62;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
 ||:|||||
 DB 13 SPIQPPEI 21

RESULT 10

AAS90616 PRELIMINARY; PRT; 62 AA.
 ID AAS90616;
 AC AAS90616;
 DT 27-APR-2004 (TrEMBLrel. 27, Created)
 DT 27-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 27-APR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative glucosamine-fructose-6-phosphate aminotransferase
 DE (Fragment).
 OS uncultured soil bacterium.
 OC Bacteria; environmental samples.
 OX NCBI_TaxID=164851;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Riesenfeld C.S., Goodman R.M., Handelsman J.;
 RT "Uncultured soil bacteria are a reservoir of new antibiotic resistance
 genes."
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

Query Match 81.2%; Score 39; DB 2; Length 292;
 Best Local Similarity 87.5%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 12

Q89QS3 PRELIMINARY; PRT; 330 AA.
 ID Q89QS3;
 AC Q89QS3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DR EMBL; AY566824; AAS90616.1; -;
 KW Amino transferase; Transferase.
 FT NON_TER 1
 SQ SEQUENCE 62 AA; 6835 MW; 4BFCBC9E94F35A4E CRC64;
 Query Match 81.2%; Score 39; DB 2; Length 62;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
 ||:|||||
 DB 13 SPIQPPEI 21

RESULT 11

DR EMBL; AY566824; AAS90616.1; -;
 KW Amino transferase; Transferase.
 FT NON_TER 1
 SQ SEQUENCE 62 AA; 6835 MW; 4BFCBC9E94F35A4E CRC64;
 Query Match 81.2%; Score 39; DB 2; Length 62;
 Best Local Similarity 66.7%; Pred. No. 22;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SPVNLPPPEL 9
 ||:|||||
 DB 13 SPIQPPEI 21

Query Match 81.2%; Score 39; DB 2; Length 292;
 Best Local Similarity 87.5%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PVNLPPPEL 9
 ||:|||||
 DB 245 PVNLPPPEL 252

RESULT 12

Q89QS3 PRELIMINARY; PRT; 330 AA.
 ID Q89QS3;
 AC Q89QS3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

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DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE B113051 protein.
GN OrderedLocusNames=b113051;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
CC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=2248498; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idegawa K., Iriiguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005946; BAC48316.1; -.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR005064; UPF0065.
DR Pfam; PF03401; Bug; 1.
DR TIGRFAMs; TIGR01409; Tat_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 330 AA; 34040 MW; 842B6CE06F95D932 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 330;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
Db 263 APKNLPPPEL 271

RESULT 13
Q9FVG6 PRELIMINARY; PRT; 854 AA.
AC Q9FVG6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Transposase.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W22; TRANSPOSON=Doppia4;
RX MEDLINE=21471138; PubMed=11587506;
RA Bercury S.D., Panavas T., Irenze K., Walker E.L.;
RT "Molecular analysis of the Dopia transposable element of maize.";
RL Plant Mol. Biol. 47:341-351(2001).
DR EMBL; AF187822; AAG17043.1; -.
DR InterPro; IPR004242; Transposase_21.
DR Pfam; PF02992; Transposase_21; 1.
SQ SEQUENCE 854 AA; 99056 MW; C3F745C5EEB706EA CRC64;

Query Match 81.2%; Score 39; DB 2; Length 854;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PVNLPPPEL 9
Db 355 PVNLPPPEL 362

RESULT 14
SNFS_YEAST STANDARD; PRT; 905 AA.
ID -SNFS_YEAST

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AC P18480;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Transcription regulatory protein SNF5 (SWI/SNF complex component SNF5)
DE (Transcription factor Tye4).
DE Name=SNF5; Synonyms=TYE4, SWI10; OrderedLocusNames=YBR289W;
GN ORFNames=YBR2036;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MCY;
RX MEDLINE=91042489; PubMed=22333708;
RA Laurent B.C., Treitel M.A., Carlson M.;
RT "The SNF5 protein of Saccharomyces cerevisiae is a glutamine- and
RT proline-rich transcriptional activator that affects expression of a
RT broad spectrum of genes.";
RL Mol. Cell. Biol. 10:5616-5625(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94378722; PubMed=8091861;
RA Holmstroem K., Brandt T., Kallioe T.;
RT "The sequence of a 32,420 bp segment located on the right arm of
RT chromosome II from Saccharomyces cerevisiae.";
RL Yeast 10:S47-S62(1994).
CC -1- FUNCTION: Involved in transcriptional activation. The SWI/SNF
CC complex is required for the induced expression of a large number
CC of genes. This complex alters chromatin structure to facilitate
CC binding of gene-specific dedicated transcription factors.
CC -1- SUBUNIT: Component of the SWI/SNF global transcription activator
CC complex.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the SNF5 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M36482; AAA35062.1; -.
DR EMBL; X76053; CAA53652.1; -.
DR EMBL; Z36158; CAA85254.1; -.
DR PIR; S44551; RGYB35.
DR IntAct; P18480; -.
DR Geronline; 138832; -.
DR SGD; S0000493; SNF5.
DR InterPro; IPR006939; SNF5.
DR Pfam; PF04855; SNF5; 1.
KW Activator; Nuclear protein; Transcription regulation.
FT DOMAIN 31 270 Gln-rich.
FT DOMAIN 72 132 Pro-rich.
FT DOMAIN 272 324 Pro-rich.
FT DOMAIN 489 588 Asp/Glu-rich (acidic).
FT DOMAIN 714 882 Pro-rich.
FT DOMAIN 755 798 Arg/Lys-rich (basic).
FT CONFLICT 564 564 E -> D (in Ref. 1).
SQ SEQUENCE 905 AA; 102557 MW; A287B4A648DDIA35 CRC64;

Query Match 81.2%; Score 39; DB 1; Length 905;
Best Local Similarity 55.6%; Pred. No. 4.1e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SPVNLPPPEL 9
Db 120 APINLPPQI 128

```



```
RESULT 15
Q9CM76
ID Q9CM76 PRELIMINARY; PRT; 1124 AA.
AC Q9CM76;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RecC.
GN Name=recC; OrderedLocusNames=PM0961;
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70."
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AB006135; AAK03045.1; -.
DR GO; GO:0009338; C:exodeoxyribonuclease V complex; IEA.
DR GO; GO:0008854; F:exodeoxyribonuclease V activity; IEA.
DR InterPro; IPR006697; RecC.
DR Pfam; PF04257; Exonuc V.gamma; 1.
DR TIGRFAMs; TIGR01450; recC; 1.
KW Complete proteome.
SQ SEQUENCE 1124 AA; 130520 MW; F249057CEPAC9C84 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 1124;
Best Local Similarity 87.5%; Pred. No. 5.2e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PVNLPPEL 9
Db 223 PVNLPPEL 230

Search completed: November 19, 2004, 23:44:27
Job time : 38.1972 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 23:28:53 ; Search time 110.028 Seconds
(without alignments)
202.141 Million cell updates/sec

Title: US-10-068-725-4_COPY_105_166

Perfect score: 315
Sequence: 1 ENKLSPVNLPELRRQSG.....SPALPLKLUSADQVALVYST 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315	100.0	166	2	Aaw75785 Human lym
2	315	100.0	166	5	Aae15494 Human TAC
3	315	100.0	246	6	Abp97720 Amino aci
4	315	100.0	246	8	Adk00762 Native hu
5	315	100.0	247	3	Aay93998 Human BR4
6	315	100.0	247	7	Abp61797 Human RYZ
7	315	100.0	265	4	Aae09244 Human TAC
8	315	100.0	266	6	Abp97723 Amino aci
9	315	100.0	293	2	Aaw75783 Human lym
10	315	100.0	293	3	Aab36312 Human neu
11	315	100.0	293	3	Aay94000 A transme
12	315	100.0	293	4	Aae09240 Human TAC
13	315	100.0	293	4	Aay71914 Human tum
14	315	100.0	293	5	Aao14130 Human tra
15	315	100.0	293	5	Abb81488 Human TAC
16	315	100.0	293	5	Aau99512 Human TAC
17	315	100.0	293	5	Aae28962 Human TAC
18	315	100.0	293	5	Aau75408 Tumour ne
19	315	100.0	293	5	Aau09900 Human AGP
20	315	100.0	293	5	Aae15493 Human tra
21	315	100.0	293	5	Abg71496 Human tum
22	315	100.0	293	6	Aae35211 Human TAC
23	315	100.0	293	6	Abp60551 Human tum
24	315	100.0	293	6	Abp97716 Amino aci
25	315	100.0	293	6	Aao29592 Human DIT

26	315	100.0	293	7	ADF72628 Human tum
27	315	100.0	293	7	Adf77379 Human tum
28	315	100.0	293	8	Adk00754 Native hu
29	315	100.0	293	8	Adj92514 Human TAC
30	315	100.0	293	8	Adn03174 Human TAC
31	315	100.0	294	8	Adk00765 hTACI epl
32	315	100.0	312	5	Aao14135 Protein o
33	310	98.4	397	5	Aae15498 Human TAC
34	300.5	95.4	291	5	Aau10949 Human AGP
35	287	91.1	404	5	Aao14136 Protein o
36	279.5	88.7	57	5	Aau10953 Human AGP
37	260	82.5	392	6	Aae35223 Human TAC
38	141.5	44.9	249	3	Aay94006 A murine
39	85	27.0	357	6	Aae35226 Human TAC
40	84.5	26.8	702	4	Abb63821 Drosophiil
41	66	21.0	428	7	Abp75685 Pseudomon
42	66	21.0	505	2	Aaw61027 Murine gu
43	66	21.0	535	2	Aaw61028 Murine gu
44	66	21.0	554	2	Aaw61026 Murine gu
45	64	20.3	88	3	Aag33433 Zea mays

ALIGNMENTS

RESULT 1
AAW75785
ID AAW75785 standard; protein; 166 AA.
XX
AC AAW75785;
XX
DT 18-JAN-1999 (first entry)
XX
DE Human lymphocyte surface receptor extracellular domain.
XX
KW TACI; transmembrane activator and CAML-interactor;
KW calcium signal-modulating cyclophilin ligand; human;
KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;
KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;
KW immunosuppressive; graft versus host disease; transplant rejection;
KW therapy; signal transduction.
XX
OS Homo sapiens.
XX
PN WO9839361-A1.
XX
PD 11-SEP-1998.
XX
PF 03-MAR-1998; 98WO-US004270.
PR 03-MAR-1997; 97US-00810572.
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI Bram RJ, Von Bulow G;
DR WPI: 1998-506346/43.
XX N-PSDB; AAV57330.
PT New isolated transmembrane activator protein - used to develop products
for treating e.g. infections, cancers, autoimmune and inflammatory
conditions, transplant rejection or graft-versus-host disease.
PS Claim 8; Page 73; 89pp; English.
CC This is the amino acid sequence of the N-terminal, i.e. the
extracellular, domain of novel human transmembrane activator and CAML-
interactor (TACI) protein (see AAW75783). TACI is a lymphocyte receptor
protein that is involved in the calcium activation pathway. It is
normally present in B-lymphocytes, and to a much lesser extent in
immature T-lymphocytes, and can therefore be targeted to specifically
regulate B cell responses without affecting T cell activity. The
extracellular domain of TACI functions as a binding site for a ligand

CC that stimulates the activation of the cell by inducing the binding of the
CC C-terminal portion (see AAW75784) of TACI to the N-terminal domain of
CC CAML. A recombinant form of the extracellular portion of TACI acts as a
CC dominant-negative or blocking agent and acts to suppress the immune
CC system. It can be used to treat or prevent autoimmune disease, graft
CC rejection or graft versus host disease. The extracellular region is also
CC used in a claimed method for identifying a ligand for TACI, in which
CC binding of a candidate molecule is determined by detecting cellular
CC activation of the AP-1, CAMP or NF- κ B pathway, of NF-AT transcription
CC factor, or of NF-AT dependent transcription
XX
SQ Sequence 166 AA;

Query Match 100.0%; Score 315; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.8e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ENKLRSPVNLPPELRRQRSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 60
DB 105 ENKLRSPVNLPPELRRQRSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 164
QY 61 ST 62
DB 165 ST 166

RESULT 2
AAE15494
ID AAE15494 standard; protein; 166 AA.
XX
AC AAE15494;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human TACI extracellular domain.
XX
KW Human; transmembrane activator and intracellular CAML interactor; TACI;
KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;
KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;
KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;
KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
KW rheumatoid arthritis; atherosclerosis.
XX
OS Homo sapiens.
XX
PN WO200187979-A2.
XX
PD 22-NOV-2001.
XX
PF 14-MAY-2001; 2001WO-US015567.
XX
PR 12-MAY-2000; 2000US-0204039P.
PR 27-JUN-2000; 2000US-0214591P.
PR 14-MAY-2001; 2001US-00214591.
XX
PA (AMGE-) AMGEN INC.
XX
XX Theill LE, Yu G;
XX WPI; 2002-066686/09.
XX
XX Inhibiting activity of B cell maturation protein and/or transmembrane
XX activator and intracellular cyclophilin ligand interactor, by
XX administering a binding partner for APRIL, a tumor necrosis factor family
XX ligand.
XX
XX Claim 1; Fig 12A; 94pp; English.
XX
XX The invention relates to a method for inhibiting TACI (transmembrane
XX activator and intracellular CAML interactor) and/or B cell maturation
XX protein (BCMA) activity in a mammal. The method comprises administering a

CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF
CC family ligand), having the consensus region of TACI, BCMA, or the TACI/
CC BCMA extracellular consensus sequence, but not the extracellular region
CC of TACI or BCMA. The method is useful for inhibiting activity of TACI
CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell
CC lymphoproliferative disorders, one or more solid tumours such as lung,
CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI
CC antagonists are useful for treating inflammation and immune function
CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic
CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung
CC disease), drug and insect sting allergy, inflammatory bowel disease
CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple
CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,
CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
CC with leucocyte infiltration of the skin or organs. The present sequence
CC is human TACI protein extracellular domain
XX
SQ Sequence 166 AA;

Query Match 100.0%; Score 315; DB 5; Length 166;
Best Local Similarity 100.0%; Pred. No. 4.8e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ENKLRSPVNLPPELRRQRSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 60
DB 105 ENKLRSPVNLPPELRRQRSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 164
QY 61 ST 62
DB 165 ST 166

RESULT 3
ABP97720
ID ABP97720 standard; protein; 246 AA.
XX
AC ABP97720;
XX
DT 28-MAY-2003 (first entry)
XX
DE Amino acid sequence of human TACI receptor.
XX
KW Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
KW TALL-1; April; systemic lupus erythematosus.
XX
OS Homo sapiens.
XX
PN WO2003014294-A2.
XX
PD 20-FEB-2003.
XX
PF 24-JUL-2002; 2002WO-US023487.
XX
PR 03-AUG-2001; 2001US-0310114P.
PR 30-APR-2002; 2002US-0377171P.
XX
PA (GETH) GENENTECH INC.
XX

PI Dixit V, Grewal I, Ridgway J, Yan M;
XX WPI; 2003-256560/25.
XX N-PSDB; AB268874.
XX
XX New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
XX preparing a composition for treating systemic lupus erythematosus.
XX
XX Disclosure; Fig 5B; 153pp; English.
XX
XX The present sequence represents a human TACI polypeptide. The
XX specification also describes BR3 polypeptides. TACI and BR3 are
XX receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April
XX bind to the TACI receptor, while TNF family ligands TALL-1 also binds to
XX BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for

CC preparing a composition for treating systemic lupus erythematosus

XX Sequence 246 AA;
 Query Match 100.0%; Score 315; DB 6; Length 246;
 Best Local Similarity 100.0%; Pred. No. 8.1e-33;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGKLKSADQVALVY 60
 |||||
 Db 59 ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGKLKSADQVALVY 118
 |||||

QY 61 ST 62
 ||
 Db 119 ST 120

RESULT 4

ADK00762
 ID ADK00762 standard; protein; 246 AA.

XX AC
 ADK00762;

DT 06-MAY-2004 (first entry)

DE Native human TACIs.

XX CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;
 KW Dermatologic; Immunosuppressive; Antiirheumatic; Antiarthritic;
 KW Antidiabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;
 KW Antibacterial; antiparasitic; systemic lupus erythematosus;
 KW diabetes mellitus; AIDS.

XX OS Homo sapiens.

XX PN WO2004011611-A2.

XX PD 05-FEB-2004.

XX PF 25-JUL-2003; 2003WO-US023421.

XX PR 25-JUL-2002; 2002US-0398530P.

XX PA (GETH) GENENTECH INC.

XX PI Chuntharapai A, Grewal I, Kim KJ, Yan M;

XX PP WPI; 2004-143841/14.

XX DR N-PSDB; ADK00761.

XX New anti-TACI receptor monoclonal antibody, useful for diagnosing and
 PT treating pathological conditions associated with tumor necrosis factor,
 PT e.g. cancer or immune-related disease, such as rheumatoid arthritis or
 PT psoriasis.

XX PS Disclosure; SEQ ID NO 14; 110pp; English.

XX The present invention relates to an isolated monoclonal antibody which
 CC binds to a transmembrane activator of and CAML interactor (TACI)
 CC receptor. The TACI antibodies are useful for modulating TALL-1 or TACI
 CC polypeptide biological activity in mammalian cells, or for diagnosing and
 CC treating pathological conditions associated with TNF and TNF receptor-
 CC related molecules, e.g. cancer or immune-related disease, such as
 CC systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome,
 CC systemic vasculitis, diabetes mellitus, Crohn's disease,
 CC glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or
 CC infectious diseases including AIDS, hepatitis infection, bacterial
 CC infection, fungal infection, protozoal infection and parasitic infection.
 CC The present sequence represents native human TACIs.

XX Sequence 246 AA;

Query Match 100.0%; Score 315; DB 8; Length 246;

Best Local Similarity 100.0%; Pred. No. 8.1e-33;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGKLKSADQVALVY 60
 |||||
 Db 59 ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGKLKSADQVALVY 118
 |||||

QY 61 ST 62

||

Db 119 ST 120

RESULT 5

AAY93998

ID AAY93998 standard; protein; 247 AA.

XX AC AAY93998;

XX DT 20-OCT-2000 (first entry)

XX DE Human BR43x2, an isoform of the TACI receptor.

XX KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasia; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Domain 1..120

FT /note= "extracellular domain"

FT Region 25..58

FT /note= "cysteine-rich pseudo repeat"

FT Domain 121..133

FT /note= "transmembrane domain"

FT Domain 134..247

FT /note= "cytoplasmic domain"

XX PN WO200040716-A2.

XX PD 13-JUL-2000.

XX PF 07-JAN-2000; 2000WO-US000396.

XX PR 07-JAN-1999; 99US-00226533.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Gross JA, Xu W, Madden K, Yee DP;

XX PP WPI; 2000-452538/39.

XX DR N-PSDB; AAA58556.

XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
 PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

XX Claim 62; Page 145; 175pp; English.

XX The present sequence represents a human BR43x2 polypeptide, which is an
 CC isoform of the transmembrane activator and CAML-interactor (TACI)
 CC receptor. TACI is a tumour necrosis factor (TNF) receptor. The
 CC extracellular domains of BR43x2, TACI or BCMA (a related B cell protein)
 CC contain a cysteine rich domain, and are used for inhibiting ztnf4
 CC activity. Ztnf4 is a TNF ligand. They may also be used for inhibiting

CC BR43x2, TAC1 or BCMA receptor-ligand engagement associated with activated
 CC or resting B lymphocytes, effector T-cells, or with antibody production.
 CC The antibody production is associated with an autoimmune disease selected
 CC from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis
 CC and rheumatoid arthritis. The ztnf4 activity and BR43x2, TAC1 or BCMA
 CC receptor-ligand engagement is associated with asthma, bronchitis,
 CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,
 CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,
 CC light chain neuropathy, amyloidosis, moderating immune response,
 CC immunosuppression, graft rejection, graft versus host disease,
 CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
 CC pain, swelling, anaemia, or septic shock. BR43x2, TAC1, and BCMA
 CC polypeptides, fusions, antibodies, agonists or antagonists can be used to
 CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol
 CC or renal emboli

XX Sequence 247 AA;

Query Match 100.0%; Score 315; DB 3; Length 247;
 Best Local Similarity 100.0%; Pred. No. 8.1e-33;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPELRRQSGVEVNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
 Db 59 ENKLRSPVNLPPELRRQSGVEVNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 118
 Qy 61 ST 62
 Db 119 ST 120

RESULT 6

ABR61797
 ID ABR61797 standard; protein; 247 AA.

XX ABR61797;

DT 12-SEP-2003 (first entry)

DE Human RYZN polypeptide.

XX RYZN; TNFRSF; tumour necrosis factor receptor; antiarteriosclerotic;
 KW type III transmembrane protein; antidiabetic; hypotensive; antilipemic;
 KW human.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Domain 1..113
 FT /note= "extracellular domain"
 FT Domain 114..136
 FT /note= "transmembrane domain"
 FT Domain 137..247
 FT /note= "intracellular domain"

XX WO2003045421-A1.

XX 05-JUN-2003.

XX 03-OCT-2002; 2002WO-IB004581.

XX 28-NOV-2001; 2001US-0334152P.

XX (GEST) GENSET SA.

XX Dyalynas D, Scalia A, Lucas J, Briggs K;

XX WPI; 2003-513616/48.

XX N-PSDB; ACC84638.

XX New agonists or antagonists of RYZN activity, useful for increasing or
 PT reducing body weight, for maintaining weight loss, and for preventing or
 PT treating an obesity-related disease or disorder, e.g. atherosclerosis or

PT diabetes.

PS Example; Page 32-33; 37pp; English.

XX The invention relates to an agonist or antagonist of RYZN activity. RYZN
 CC is a member of the Tumour Necrosis Factor Receptor Super Family (TNFRSF)
 CC and is a Type III transmembrane protein. The agonist or antagonist of
 CC RYZN activity, or compositions comprising them is useful for preventing
 CC or treating an obesity-related disease or disorder, such as insulin
 CC resistance, hyperlipidemia, atherosclerosis, diabetes, hypertension,
 CC syndrome X, and hyperuricemia. These may also be used to increase or
 CC reduce body weight, or maintain weight loss. The present sequence
 CC represents the human RYZN polypeptide

XX Sequence 247 AA;

Query Match 100.0%; Score 315; DB 7; Length 247;
 Best Local Similarity 100.0%; Pred. No. 8.1e-33;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPELRRQSGVEVNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
 Db 59 ENKLRSPVNLPPELRRQSGVEVNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 118
 Qy 61 ST 62
 Db 119 ST 120

RESULT 7

AAE09244
 ID AAE09244 standard; protein; 265 AA.

XX AAE09244;

XX 19-NOV-2001 (first entry)

DE Human TAC1 splice variant protein.

XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
 KW TAC1; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.

XX Homo sapiens.

XX WO200160397-A1.

XX 23-AUG-2001.

XX 28-NOV-2000; 2000WO-US032378.

XX 16-FEB-2000; 2000US-0182938P.

XX 22-AUG-2000; 2000US-0226986P.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
 PI Yan M;

XX WPI; 2001-541628/60.

XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity, for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists.

XX Example 1; Fig 6; 160pp; English.

XX The invention relates to methods of using one or more agonists or
 CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
 CC TAC1 or BCMA. The method is useful for treating pathological conditions
 CC or diseases associated with increased TALL-1 and APRIL expression or

CC activity, TALL-1 and APRIL antagonists are used to block the interaction
CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid
CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
CC present sequence is human TACI splice variant protein
XX
XX
SQ Sequence 265 AA;

Query Match 100.0%; Score 315; DB 4; Length 265;
Best Local Similarity 100.0%; Pred. No. 8.9e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSFVNLPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
DB 105 ENKLRSFVNLPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
DB 165 ST 166

RESULT 8
ABP97723
ID ABP97723 standard; protein; 266 AA.
XX
AC ABP97723;
XX
DT 28-MAY-2003 (first entry)
XX
DE Amino acid sequence of an alternatively spliced human TACI receptor.
XX
KW Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;
KW TALL-1; April; systemic lupus erythematosus.
XX
OS Homo sapiens.
XX
PN WO2003014294-A2.
XX
PD 20-FEB-2003.
XX
PF 24-JUL-2002; 2002WO-US023487.
XX
PR 03-AUG-2001; 2001US-0310114P.
PR 30-APR-2002; 2002US-0377171P.
XX
PA (GETH) GENENTECH INC.
XX
PI Dixit V, Grewal I, Ridgway J, Yan M;
XX
DR WPI; 2003-256560/25.
XX

PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for
PT preparing a composition for treating systemic lupus erythematosus.
XX
PS Disclosure; Fig 8; 153pp; English.

CC The present sequence represents an alternatively spliced human TACI
CC polypeptide. The specification also describes BR3 polypeptides. TACI and
CC BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and
CC April bind to the TACI receptor, while TNF family ligands TALL-1 also
CC binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful
CC for preparing a composition for treating systemic lupus erythematosus
XX
XX
SQ Sequence 266 AA;

Query Match 100.0%; Score 315; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 9e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSFVNLPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
DB 105 ENKLRSFVNLPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
DB 165 ST 166

RESULT 9
AAW75783
ID AAW75783 standard; protein; 293 AA.
XX
AC AAW75783;
XX
DT 18-JAN-1999 (first entry)
XX
DE Human lymphocyte surface receptor TACI.
XX
KW TACI; transmembrane activator and CAML-interactor;
KW calcium signal-modulating cyclophilin ligand; human;
KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;
KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;
KW immunosuppressive; graft versus host disease; transplant rejection;
KW therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..166
FT /label= Extracellular_domain
FT /note= "Claim 8"
FT Peptide 34..71
FT /note= "TNFR_NGFR motif"
FT Domain 167..186
FT /label= Transmembrane_domain
FT Domain 187..294
FT /label= Cytoplasmic_domain
FT /note= "Claim 6"
XX
PN WO9839361-A1.
XX
PD 11-SEP-1998.
XX
PF 03-MAR-1998; 98WO-US004270.
XX
PR 03-MAR-1997; 97US-00810572.
XX
PA (SUJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
XX
PI Bram RJ, Von Bulow G;
XX
DR WPI; 1998-506346/43.
DR N-PSDB; AAV57328.
XX
PT New isolated transmembrane activator protein - used to develop products
PT for treating e.g. infections, cancers, autoimmune and inflammatory
PT conditions, transplant rejection or graft-versus-host disease.
XX
PS Claim 20; Fig 2a; 89pp; English.

CC This is the amino acid sequence of novel human transmembrane activator
CC and CAML-interactor (TACI) protein, a lymphocyte receptor protein that is
CC involved in the calcium activation pathway. TACI is normally present in B
CC -lymphocytes, and to a much lesser extent in immature T-lymphocytes, and
CC can therefore be targeted to specifically regulate B cell responses
CC without affecting T cell activity. TACI cDNA (seeV57328) was isolated
CC from a B-lymphocyte cDNA library using a yeast two-hybrid assay. Also
CC claimed are the C-terminal (see AAW75784) and N-terminal (see AAW75785)
CC fragments of TACI, recombinant DNA constructs, unicellular hosts, and
CC antibodies to TACI protein. Methods are claimed for identifying a ligand
CC for TACI and for identifying immunosuppressive drugs that selectively
CC block the action of B lymphocytes without affecting mature T lymphocytes.
CC TACI can be activated to increase immune system activity, e.g. for
CC treating infections or cancers. It can be blocked to provide
CC immunosuppression, e.g. for treating autoimmune and inflammatory

CC conditions such as immune complex- induced vasculitis.
 CC glomerulonephritis, haemolytic anaemia, myasthenia gravis, type II
 CC collagen-induced arthritis, experimental allergic and hyperacute
 CC xenograft rejection, rheumatoid arthritis, systemic lupus erythematosus,
 CC transplant rejection, cancer or graft versus host disease
 XX

SQ Sequence 293 AA;
 Query Match 100.0%; Score 315; DB 2; Length 293;
 Best Local Similarity 100.0%; Pred. No. 1e-32;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 60
 DB 105 ENKLSPVNLPPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 164
 QY 61 ST 62
 DB 165 ST 166

RESULT 10
 AAB36312
 ID AAB36312 standard; protein; 293 AA.
 XX
 AC AAB36312;
 DT 26-FEB-2001 (first entry)
 XX
 DE Human neutrokin-alpha binding protein TR17 SEQ ID NO:2.
 KW Human; neutrokin-alpha binding protein; NAR protein; TR17; cytostatic;
 KW immunosuppressive; neutrotropic; neuroprotective; antiviral; anti-allergic;
 KW hepatotropic; antidiabetic; anti-inflammatory; antitumor; cardiant;
 KW ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;
 KW autoimmune disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200058362-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007966.
 XX
 PR 26-MAR-1999; 99US-0126599P.
 PR 10-MAR-2000; 2000US-0188208P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ullrich S, Baker K;
 XX
 DR WPI; 2000-602359/57.
 DR N-PSDB; AAC64602.
 XX
 PT Nucleic acid encoding a neutrokin-alpha receptor (NAR) such as TR17,
 PT useful for producing TR17 protein which is used in the treatment and
 PT diagnosis of autoimmune and immunodeficiency disorders.
 XX
 PS Claim 1; Fig 1; 398pp; English.
 XX
 CC The present sequence represents the human neutrokin-alpha binding (NAR)
 CC protein designated TR17. TR17 has cytostatic, immunosuppressive,
 CC neutrotropic, neuroprotective, antiviral, anti-allergic, hepatotropic,
 CC antidiabetic, anti-inflammatory, antitumor, cardiant and ophthalmological
 CC activities and can be used in gene therapy. The TR17 protein and
 CC antibodies are useful for treating and diagnosing immunodeficiency
 CC disorders and autoimmune disorders. The TR17 polypeptides,
 CC polynucleotides, antibodies, agonists and/or antagonists are used for
 CC treating various other diseases defined in the specification and as
 CC research tools for studying the phenotypic effects that result from
 CC inhibiting TR17/TR17 ligand interactions on various cell types
 XX

SQ Sequence 293 AA;
 Query Match 100.0%; Score 315; DB 3; Length 293;
 Best Local Similarity 100.0%; Pred. No. 1e-32;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 60
 DB 105 ENKLSPVNLPPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 164
 QY 61 ST 62
 DB 165 ST 166

RESULT 11
 AAY94000
 ID AAY94000 standard; protein; 293 AA.
 XX
 AC AAY94000;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE A transmembrane activator and CAML-interactor (TACI).
 XX
 KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;
 KW immune response; immunosuppression; graft rejection; joint pain;
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.
 XX
 OS Homo sapiens.
 XX
 PN WO200040716-A2.
 XX
 PD 13-JUL-2000.
 XX
 PF 07-JAN-2000; 2000WO-US000396.
 XX
 PR 07-JAN-1999; 99US-00226533.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Gross JA, Xu W, Madden K, Yee DP;
 XX
 DR WPI; 2000-452538/39.
 DR N-PSDB; AAS58558.
 XX
 PT Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,
 PT renal disease, graft versus host disease, and inflammation, comprises
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
 XX
 PS Disclosure; Page 149-150; 175pp; English.
 XX
 CC The present sequence represents a human transmembrane activator and CAML-
 CC interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF)
 CC receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI
 CC or BCMA (a related B cell protein) receptor contain a cysteine rich
 CC domain, and are used for inhibiting ztnf4 activity. Ztnf4 is a TNF
 CC ligand. They may also be used for inhibiting BR43x2, TACI or BCMA
 CC receptor-ligand engagement associated with activated or resting B
 CC lymphocytes, effector T-cells, or with antibody production. The antibody
 CC production is associated with an autoimmune disease selected from
 CC systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and
 CC rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA
 CC receptor-ligand engagement is associated with asthma, bronchitis,
 CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,
 CC

CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,
 CC light chain neuropathy, amyloidosis, moderating immune response,
 CC immunosuppression, graft rejection, graft versus host disease,
 CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint
 CC pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA
 CC polypeptides, fusions, antibodies, agonists or antagonists can be used to
 CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol
 CC or renal emboli
 XX
 SQ Sequence 293 AA;

Query Match 100.0%; Score 315; DB 3; Length 293;
 Best Local Similarity 100.0%; Pred. No. 1e-32;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENKLRSPVNLPELRQRSGEVENNSDGRYQGLEHRCSEASPALPGLKLSADQVALVY 60
 DB 105 ENKLRSPVNLPELRQRSGEVENNSDGRYQGLEHRCSEASPALPGLKLSADQVALVY 164
 QY 61 ST 62
 DB 165 ST 166

RESULT 12
 ID AAE09240
 AC AAE09240;
 DT 19-NOV-2001 (first entry)
 DE Human TACI protein.
 KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
 KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
 XX
 OS Homo sapiens.

XX
 XX WO200160397-A1.
 XX 23-AUG-2001.
 XX 28-NOV-2000; 2000WO-US032378.
 XX 16-FEB-2000; 2000US-0182938P.
 XX 22-AUG-2000; 2000US-0226986P.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
 XX Yan M;
 XX WPI; 2001-541628/60.
 XX N-PSDB; AAD15901.

XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
 PT activity, for treating autoimmune disorders and cancer, comprises
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
 PT antagonists.

XX Example 1; Fig 1; 160pp; English.

XX The invention relates to methods of using one or more agonists or
 CC antagonists to modulate the activity of the members of TNF (tumour
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.
 CC TACI or BCMA. The method is useful for treating pathological conditions
 CC or diseases associated with increased TALL-1 and APRIL expression or
 CC activity. TALL-1 and APRIL antagonists are used to block the interaction
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid

CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The
 CC present sequence is human TACI protein
 XX
 SQ Sequence 293 AA;

Query Match 100.0%; Score 315; DB 4; Length 293;
 Best Local Similarity 100.0%; Pred. No. 1e-32;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPELRQRSGEVENNSDGRYQGLEHRCSEASPALPGLKLSADQVALVY 60
 DB 105 ENKLRSPVNLPELRQRSGEVENNSDGRYQGLEHRCSEASPALPGLKLSADQVALVY 164
 QY 61 ST 62
 DB 165 ST 166

RESULT 13
 ID AAY71914
 AC AAY71914;
 DT 26-MAR-2001 (first entry)
 DE Human tumour necrosis factor receptor (TACI) protein.
 KW Human; transmembrane activator and CAML interactor; TACI;
 KW tumour necrosis factor receptor; TNF; autoimmune disease; diabetes;
 KW calcium-signal modulating cyclophilin ligand; CAML; viral infection;
 KW neutrokin alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy;
 KW neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour;
 KW antiarthritic; antirheumatic; immunosuppressive; multiple sclerosis;
 KW rheumatoid arthritis; graft rejection; inflammation; cell proliferation;
 KW cell death; immunoglobulin E-mediated allergic reaction; IgE.

XX Homo sapiens.

XX
 XX Key Location/Qualifiers
 FT Domain 2..166
 FT /label= Extracellular domain
 FT /note= "Binds with amino acids 123-285 of extracellular
 FT domain of TACI-L"

XX WO2000067034-A1.

XX 09-NOV-2000.

XX 14-APR-2000; 2000WO-US010282.

XX 30-APR-1999; 99US-00302863.

XX (IMMV) IMMUNEX CORP.

XX Goodwin RG, Din WS;

XX WPI; 2001-016005/02.

XX N-PSDB; AAD02006.

XX Use of new interactions between tumor necrosis factor receptors (TACI)
 PT and TACI ligands to screen candidate molecules for determining agonist
 PT and antagonist interactions which are used for treating inflammation.

XX Claim 10; Fig 1b; 45pp; English.

XX The present sequence is a human tumour necrosis factor receptor (TACI)
 CC protein. TACI (Transmembrane activator and calcium-signal modulating
 CC cyclophilin ligand (CAML)-interactor) forms a complex with neutrokin
 CC alpha polypeptide (TACI-Ligand). The antagonist or agonist of TACI/TACI-L
 CC complex is useful for modulating an intracellular signalling cascade
 CC mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L complex are
 CC used to inhibit the interaction between TACI and TACI-L for therapeutic

CC purposes to treat tumour and tumour metastasis and to combat various
 CC autoimmune diseases e.g. multiple sclerosis and diabetes, as well as
 CC other disorders, such as viral infection, rheumatoid arthritis, graft
 CC rejection, and immunoglobulin (Ig) E-mediated allergic reactions and
 CC inflammation. The interaction is used to study cellular processes
 CC associated with tumour necrosis factor (TNF)-receptors such as immune
 CC regulation, cell proliferation, cell death and inflammatory responses.
 CC The interaction between the extracellular region of TACI and TACI-L can
 CC be used to further develop understanding of which cell types TACI-L acts
 CC upon
 XX
 SQ Sequence 293 AA;

Query Match 100.0%; Score:315; DB 4; Length 293;
 Best Local Similarity 100.0%; Pred. No.1e-32;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 60
 DB |||||
 105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 164
 QY 61 ST 62
 ||
 DB 165 ST 166

RESULT 14
 AAO14130
 ID AAO14130 standard; protein; 293 AA.
 XX
 AC AAO14130;
 DT 02-MAY-2002 (first entry)
 XX
 DE Human transmembrane activator CAML interactor protein (TACI).
 XX
 KW Human transmembrane activator CAML interactor protein; TACI; cytostatic;
 KW cell proliferation; tumour; vulvar; renal cell cancer; mastocytoma;
 KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
 KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
 KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
 KW scleroderma; rheumatoid arthritis; scarring; liver; lung fibrosis;
 KW uterine.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..114
 FT /label= Extracellular_domain
 XX
 PN WO200181417-A2.
 XX
 PD 01-NOV-2001.
 XX
 XX 27-APR-2001; 2001WO-US040626.
 XX
 XX 27-APR-2000; 2000US-0199946P.
 XX
 XX (BIOJ) BIOGEN INC.
 XX (APOT-) APOTEC R & D SA.
 XX
 PI Ambrose C, Thompson J, Schneider P, Rennert P;
 XX
 DR WPI; 2002-062027/08.
 DR N-PSDB; AAK98726.
 XX
 XX Treating mammal for condition associated with undesired cell
 XX proliferation e.g., solid tumor or reducing solid tumor size located in
 XX mammal comprises administering transmembrane activator CAML interactor
 XX protein reagent.
 XX
 XX Claim 8; Fig 1; 42pp; English.
 PS
 XX

CC This sequence represents the human transmembrane activator CAML
 CC interactor protein (TACI). The invention relates to treating a mammal for
 CC a condition associated with undesired cell proliferation (e.g. a solid
 CC tumour, or reducing the size of a solid tumour located on or in a mammal)
 CC comprising administering a transmembrane activator CAML interactor
 CC protein (TACI) reagent. The TACI reagent has cytostatic and vulnerary
 CC activity. Treating a mammal (e.g. human, cow, horse, dog, mouse, rat or
 CC cat) for a condition associated with undesired cell proliferation (e.g.
 CC cancer such as renal cell cancer, Kaposi's sarcoma, breast cancer,
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon
 CC cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma,
 CC pharyngeal squamous cell carcinoma, gastrointestinal cancer or stomach
 CC cancer). The method is also useful for treating cellular
 CC hyperproliferation (hyperplasia) such as scleroderma, pannus formation in
 CC rheumatoid arthritis, post-surgical scarring and lung, liver and uterine
 CC fibrosis. The TACI reagent of the invention can extend mean survival time
 CC of a mammal by 25% as compared to the mean survival time of a mammal in
 CC the absence of administering the TACI reagent. The TACI reagent also
 CC reduces the size of the tumour by 25% or more
 XX
 SQ Sequence 293 AA;

Query Match 100.0%; Score 315; DB 5; Length 293;
 Best Local Similarity 100.0%; Pred. No.1e-32;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 60
 DB |||||
 105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 164
 QY 61 ST 62
 ||
 DB 165 ST 166

RESULT 15
 ABB81488
 ID ABB81488 standard; protein; 293 AA.
 XX
 AC ABB81488;
 XX
 DT 02-SBP-2002 (first entry)
 XX
 DE Human TACI receptor related protein SEQ ID NO:8.
 XX
 KW Human; Tnfr12; tumour necrosis factor receptor; cytostatic;
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;
 KW light chain neuropathy; hypertension; large vessel disease;
 KW graft-versus host disease; graft rejection; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200238766-A2.
 XX
 XX 16-MAY-2002.
 XX
 XX 05-NOV-2001; 2001WO-US047018.
 XX
 XX 07-NOV-2000; 2000US-0246449P.
 XX
 XX 20-DEC-2000; 2000US-0257131P.
 XX
 XX 28-JUN-2001; 2001US-0301715P.
 XX
 XX 29-AUG-2001; 2001US-0315565P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Gross JA, Xu W, Henne RM, Grant FJ;
 PI

XX WPI; 2002-508212/54.
XX
XX Novel isolated human tumor necrosis factor receptor polypeptide, termed
PT Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
PT renal failure or renal disease and lymphoma.
XX
XX
PS Disclosure; Page 136-137; 154pp; English.
XX
XX The present invention describes a human tumour necrosis factor receptor
CC designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive,
CC dermatological, antiinflammatory, neuroprotective, antidiabetic,
CC antirheumatic, antiarthritic, antiasthmatic, nephrotropic and hypotensive
CC activities, and can be used in gene therapy. (I) can be used for
CC inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12
CC (e.g. ZTNF4), for treating disorders and diseases associated with B
CC lymphocytes, activated B lymphocytes or resting B lymphocytes, and for
CC inhibiting the proliferation of tumour cells. (I) is useful for treating
CC autoimmune disorders such as systemic lupus erythematosus, myasthenia
CC gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma,
CC rheumatoid arthritis, bronchitis, emphysema and end stage renal failure
CC or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
CC leukaemia, nephritis, and pyelonephritis, and for treating renal
CC neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or
CC amyloidosis, hypertension, large vessel diseases, graft-versus host
CC disease, graft rejection and Crohn's disease. (I) is useful for
CC modulating the immune system, for regulating B cell responses and
CC development, for modulating development of other cells, antibody
CC production and cytokine production, and for modulating T and B cell
CC communication. The present sequence represents a protein which is given
CC in the exemplification of the present invention
XX
SQ Sequence 293 AA;

Query Match 100.0%; Score 315; DB 5; Length 293;
Best Local Similarity 100.0%; Pred. No. 1e-32; Mismatches 0; Indels 0; Gaps 0;
Matches 62; Conservative 0;
QY 1 ENKLSPVNLPELRRQSGEVENNSDNGRYQGLEHRCSEASPALPGLKLSADQVALVY 60
Db 105 ENKLSPVNLPELRRQSGEVENNSDNGRYQGLEHRCSEASPALPGLKLSADQVALVY 164
QY 61 ST 62
Db 165 ST 166

Search completed: November 19, 2004, 23:40:02
Job time : 114.028 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 23:37:09 ; Search time 48.9014 Seconds
(without alignments)
84.082 Million cell updates/sec

Title: US-10-068-725-4_COPY_105_166

Perfect score: 315

Sequence: 1 ENKLSPVNLPELRQRSG.....SPALPGLKLSADQVALVYST 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS-COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	315	100.0	166	2	US-08-810-572A-6
2	315	100.0	166	3	US-09-290-333-6
3	315	100.0	166	4	US-09-782-857A-6
4	315	100.0	166	4	US-09-854-864-15
5	315	100.0	293	2	US-08-810-572A-2
6	315	100.0	293	3	US-09-290-333-2
7	315	100.0	293	4	US-09-782-857A-2
8	315	100.0	293	4	US-09-879-919-22
9	315	100.0	293	4	US-09-848-295-4
10	315	100.0	293	4	US-09-854-864-14
11	310	98.4	397	4	US-09-854-864-18
12	66	21.0	428	4	US-09-252-991A-24431
13	64	20.3	328	4	US-09-252-991A-3205
14	64	20.3	341	4	US-09-252-991A-18308
15	62	19.7	179	4	US-09-252-991A-30669
16	62	19.7	635	4	US-09-252-991A-21514
17	62	19.7	806	1	US-07-980-528-2
18	62	19.7	824	4	US-09-538-092-1242
19	61	19.4	412	4	US-09-252-991A-30252
20	61	19.4	487	4	US-09-248-796A-19251
21	60.5	19.2	336	4	US-09-252-991A-22196
22	60.5	19.2	954	4	US-09-252-991A-32931
23	60	19.0	349	3	US-09-343-011B-1
24	60	19.0	487	4	US-09-252-991A-18581
25	59.5	18.9	203	4	US-09-134-000C-6471
26	59	18.7	242	4	US-09-270-767-43590
27	59	18.7	710	3	US-09-079-812E-2

28	58.5	18.6	214	4	US-09-252-991A-22902	Sequence 22902, A
29	58.5	18.6	261	4	US-09-252-991A-28545	Sequence 28545, A
30	58.5	18.6	453	4	US-09-270-767-44670	Sequence 44670, A
31	58.5	18.6	693	4	US-09-252-991A-24059	Sequence 24059, A
32	58	18.4	511	4	US-09-198-452A-509	Sequence 509, App
33	58	18.4	621	3	US-09-026-343-7	Sequence 7, Appli
34	58	18.4	621	3	US-09-362-871-7	Sequence 7, Appli
35	58	18.4	1385	2	US-08-687-399-7	Sequence 7, Appli
36	57.5	18.3	190	4	US-09-270-767-46639	Sequence 46639, A
37	57.5	18.3	362	4	US-09-252-991A-30223	Sequence 30223, A
38	57.5	18.3	385	4	US-09-252-991A-25080	Sequence 25080, A
39	57.5	18.3	584	4	US-09-270-767-43419	Sequence 43419, A
40	57	18.1	179	4	US-09-252-991A-25298	Sequence 25298, A
41	57	18.1	213	4	US-09-252-991A-32093	Sequence 32093, A
42	57	18.1	230	4	US-09-252-991A-17268	Sequence 17268, A
43	57	18.1	258	4	US-09-252-991A-31620	Sequence 31620, A
44	57	18.1	430	1	US-08-035-392-4	Sequence 4, Appli
45	57	18.1	430	1	US-08-504-511A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-810-572A-6

Query Match 100.0%; Score 315; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.1e-34;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPPLRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPPLRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62
Db 165 ST 166

RESULT 2
US-09-290-333-6
; Sequence 6, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-290-333-6

Query Match 100.0%; Score 315; DB 3; Length 166;
Best Local Similarity 100.0%; Pred. No. 7,1e-34;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPPLRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPPLRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62
Db 165 ST 166

RESULT 3
US-09-782-857A-6
; Sequence 6, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-857A-6

Query Match 100.0%; Score 315; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 7,1e-34;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPPLRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPPLRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62
Db 165 ST 166

RESULT 4
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

;
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-854-864-15

Query Match 100.0%; Score 315; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 7.1e-34; Indels 0; Gaps 0;
Matches 62; Conservative 0; Mismatches 0;
QY 1 ENKLSPVNLPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
Db 105 ENKLSPVNLPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
Db 165 ST 166

RESULT 5
US-08-810-572A-2
; Sequence 2, Application US/08810572A
; Patent No. 5969102
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,572A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal

;
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-810-572A-2
Query Match 100.0%; Score 315; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.5e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ENKLSPVNLPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
Db 105 ENKLSPVNLPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
Db 165 ST 166

RESULT 6
US-09-290-333-2
; Sequence 2, Application US/09290333
; Patent No. 6316222
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/290,333
; FILING DATE: 12-Apr-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-290-333-2

Query Match 100.0%; Score 315; DB 3; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.5e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ENKLSPVNLPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
Db 105 ENKLSPVNLPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62
Db 165 ST 166

RESULT 7
US-09-782-857A-2
; Sequence 2, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical TYPE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-857A-2

Query Match 100.0%; Score 315; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.5e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPELRRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPELRRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62
Db 165 ST 166

RESULT 8
US-09-879-919-22

Query Match 100.0%; Score 315; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.5e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPELRRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPELRRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

; Sequence 22, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 22
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-22

Query Match 100.0%; Score 315; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.5e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPELRRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPELRRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62
Db 165 ST 166

RESULT 9
US-09-848-295-4
; Sequence 4, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
; THEREON
; FILE REFERENCE: PF527
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-295-4

Query Match 100.0%; Score 315; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.5e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPELRRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPELRRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

Db 105 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 164
QY 61 ST 62
Db 165 ST 166

RESULT 10
US-09-854-864-14
; Sequence 14, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-14

Query Match 100.0%; Score 315; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.5e-33;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
Db 165 ST 166

RESULT 11
US-09-854-864-18
; Sequence 18, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-18

Query Match 98.4%; Score 310; DB 4; Length 397;
Best Local Similarity 100.0%; Pred. No. 1e-32;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 60

Db 105 ENKLRSPVNLPELRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 164
QY 61 S 61
Db 165 S 165

RESULT 12
US-09-252-991A-24431
; Sequence 24431, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24431
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24431

Query Match 21.0%; Score 66; DB 4; Length 428;
Best Local Similarity 40.9%; Pred. No. 2.3;
Matches 18; Conservative 8; Mismatches 8; Indels 10; Gaps 2;

QY 14 LRRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVA 57
Db 254 LAQQAGHROQH-----HEGLE-----EAHPAFDLLLLADQVA 287

RESULT 13
US-09-252-991A-23205
; Sequence 23205, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23205
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23205

Query Match 20.3%; Score 64; DB 4; Length 328;
Best Local Similarity 31.8%; Pred. No. 3;
Matches 21; Conservative 8; Mismatches 23; Indels 14; Gaps 3;

QY 6 SPVN--LPPELRRQRSGEVENNSDNGRYQGL-----EHRGSEASPALPGLKLS 52
Db 165 APVGAALPPAARRQRTGPA--GGGHRDGRRTALGVFALRRRDLPDFPGCARPGLOGIEQA 223

QY 53 ADQVAL 58
Db 224 AHRVAV 229

RESULT 14

US-09-252-991A-18308
; Sequence 18308, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18308
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18308

Query Match 20.3%; Score 64; DB 4; Length 341;
Best Local Similarity 30.5%; Pred. No. 3.2;
Matches 18; Conservative 7; Mismatches 20; Indels 14; Gaps 2;
Qy 9 NLPPELR-----QRGEVNNDSNGRYQGLEHRSSEASPALFGLKLSADQ 55
Db 144 HLPYRRRAQRAARGPERPORTG--RHGPDRAHRRPQHRGTAVGRLPAATVERDQ 200

RESULT 15

US-09-252-991A-30669
; Sequence 30669, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30669
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30669

Query Match 19.7%; Score 62; DB 4; Length 179;
Best Local Similarity 41.3%; Pred. No. 2.5;
Matches 19; Conservative 4; Mismatches 19; Indels 4; Gaps 2;
Qy 10 LPPELRQRGEVNNDSNGRY--QGLEHRSSEASPALFGLKLSA 53
Db 91 LHPQLRRQRPAAHFGTTERDRRCQDQGLRRPFGCAD--LPQLRSQA 134

Search completed: November 19, 2004, 23:45:54
Job time : 50.9014 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 23:40:10 ; Search time 168.535 Seconds
(without alignments)
130.275 Million cell updates/sec

Title: US-10-068-725-4_COPY_105_166

Perfect score: 315

Sequence: 1 ENKLRSPVNLPELRQRSG.....SPALPGLKLSADQVALVYST 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	315	100.0	166	9 US-09-854-864-15	Sequence 15, Appl
2	315	100.0	166	9 US-09-855-158-15	Sequence 15, Appl
3	315	100.0	166	14 US-10-293-816-6	Sequence 22, Appl
4	315	100.0	293	9 US-09-879-919-22	Sequence 6, Appl
5	315	100.0	293	9 US-09-854-864-14	Sequence 14, Appl
6	315	100.0	293	9 US-09-855-158-14	Sequence 14, Appl
7	315	100.0	293	9 US-09-961-376-2	Sequence 2, Appl
8	315	100.0	293	9 US-09-779-050A-42	Sequence 42, Appl
9	315	100.0	293	10 US-09-302-863-2	Sequence 2, Appl
10	315	100.0	293	10 US-09-855-564-2	Sequence 2, Appl
11	315	100.0	293	13 US-10-087-192-1650	Sequence 1650, Ap
12	315	100.0	293	13 US-10-084-971-2	Sequence 2, Appl
13	315	100.0	293	14 US-10-068-725-4	Sequence 4, Appl

14	315	100.0	293	14	US-10-151-882-46	Sequence 46, Appl
15	315	100.0	293	14	US-10-293-816-2	Sequence 2, Appl
16	315	100.0	293	14	US-10-008-063-8	Sequence 8, Appl
17	315	100.0	293	14	US-10-152-363A-2	Sequence 2, Appl
18	315	100.0	293	14	US-10-268-951-22	Sequence 22, Appl
19	315	100.0	293	15	US-10-258-368-1	Sequence 1, Appl
20	315	100.0	293	15	US-10-618-797-4	Sequence 4, Appl
21	315	100.0	293	17	US-10-742-634-7	Sequence 7, Appl
22	315	100.0	293	17	US-10-748-112-27	Sequence 27, Appl
23	315	100.0	301	15	US-10-258-368-12	Sequence 12, Appl
24	310	98.4	397	9	US-09-854-864-18	Sequence 18, Appl
25	310	98.4	397	9	US-09-855-158-18	Sequence 18, Appl
26	300.5	95.4	291	9	US-09-779-050A-43	Sequence 43, Appl
27	287	91.1	404	15	US-10-258-368-15	Sequence 15, Appl
28	279.5	88.7	57	9	US-09-779-050A-47	Sequence 47, Appl
29	260	82.5	392	14	US-10-152-363A-50	Sequence 50, Appl
30	141.5	44.9	249	13	US-10-087-192-1647	Sequence 1647, Ap
31	85	27.0	357	14	US-10-152-363A-56	Sequence 56, Appl
32	68	21.6	305	15	US-10-424-599-181850	Sequence 181850,
33	66	21.0	505	16	US-10-437-963-103271	Sequence 103271,
34	66	21.0	554	9	US-09-746-491-41	Sequence 41, Appl
35	65	20.6	112	17	US-10-425-115-199566	Sequence 199566,
36	64.5	20.5	402	15	US-10-425-114-63733	Sequence 63733, A
37	64.5	20.5	403	15	US-10-425-114-63734	Sequence 63734, A
38	64.5	20.5	404	15	US-10-425-114-42053	Sequence 42053, A
39	64	20.3	433	16	US-10-437-963-106971	Sequence 106971,
40	64	20.3	448	16	US-10-437-963-107712	Sequence 107712,
41	64	20.3	1028	15	US-10-424-599-171115	Sequence 171115,
42	63.5	20.2	148	16	US-10-437-963-192537	Sequence 192537,
43	63	20.0	109	17	US-10-425-115-222291	Sequence 222291,
44	63	20.0	1489	15	US-10-343-710-96	Sequence 96, Appl
45	62.5	19.8	542	17	US-10-425-115-240726	Sequence 240726,

ALIGNMENTS

RESULT 1
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-686B
; CURRENT APPLICATION NUMBER: US/09/854, 864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-15

Query Match	100.0%	Score 315;	DB 9;	Length 166;
Best Local Similarity	100.0%	Pred. No. 1.5e-30;		
Matches	62;	Conservative	0;	Mismatches 0;
			Indels	0; Gaps 0;
QY	1	ENKLRSPVNLPELRQRSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY	60	
Db	105	ENKLRSPVNLPELRQRSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY	164	
QY	61	ST 62		
Db	165	ST 166		

US-09-854-864-14

Query Match 100.0%; Score 315; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
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Db 105 ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
||
Db 165 ST 166

RESULT 6

US-09-855-158-14
; Sequence 14, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-14

Query Match 100.0%; Score 315; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
|||||
Db 105 ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
||
Db 165 ST 166

RESULT 7

US-09-961-376-2
; Sequence 2, Application US/09961376
; Patent No. US20020106736A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17
; FILE REFERENCE: PF524F1
; CURRENT APPLICATION NUMBER: US/09/961,376
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/254,874
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/235,991
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: 09/533,822
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-961-376-2

Query Match 100.0%; Score 315; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
|||||
Db 105 ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
||
Db 165 ST 166

RESULT 8

US-09-779-050A-42
; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

Query Match 100.0%; Score 315; DB 9; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
|||||
Db 105 ENKLSPVNLPELRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
||
Db 165 ST 166

RESULT 9

US-09-302-863-2
; Sequence 2, Application US/09302863
; Publication No. US2003002223A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; APPLICANT: Din, Wanwan S.
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-09-302-863-2

Query Match 100.0%; Score 315; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164
Qy 61 ST 62
Db 165 ST 166

RESULT 10
US-09-855-564-2
; Sequence 2, Application US/09855564
; Publication No. US20030165986A1
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/855,564
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/302,863
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Human
US-09-855-564-2

Query Match 100.0%; Score 315; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164
Qy 61 ST 62
Db 165 ST 166

RESULT 11
US-10-087-192-1650
; Sequence 1650, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 52945200122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1650
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-1650

Query Match 100.0%; Score 315; DB 13; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164
Qy 61 ST 62
Db 165 ST 166
RESULT 12
US-10-084-971-2
; Sequence 2, Application US/10084971
; Publication No. US20020187526A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Neurokine-alpha Binding Proteins and Methods Based Thereon
; FILE REFERENCE: PF524PCT
; CURRENT APPLICATION NUMBER: US/10/084,971
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/533,822
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/188,208
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-084-971-2

Query Match 100.0%; Score 315; DB 13; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164
Qy 61 ST 62
Db 165 ST 166

RESULT 13
US-10-068-725-4
; Sequence 4, Application US/10068725
; Publication No. US20030012783A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
; FILE REFERENCE: 01-04
; CURRENT APPLICATION NUMBER: US/10/068,725
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/270,274
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/283,447
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-725-4

Query Match 100.0%; Score 315; DB 14; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ENKLRSPVNLPPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60

Db 105 ENKLRSPVNLPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164
Qy 61 ST 62
Db 165 ST 166

RESULT 14
US-10-151-882-46
; Sequence 46, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-46

Query Match 100.0%; Score 315; DB 14; Length 293;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ENKLRSPVNLPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60
Db 105 ENKLRSPVNLPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164
Qy 61 ST 62
Db 165 ST 166

RESULT 15
US-10-293-816-2
; Sequence 2, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Goetz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-2

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Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ENKLRSPVNLPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60

Db 105 ENKLRSPVNLPELRRQSRGSEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164
Qy 61 ST 62
Db 165 ST 166

Search completed: November 20, 2004, 00:00:28
Job time : 172.535 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	62.5	19.8	1741	2	T13610	parallel sister ch
2	62.5	19.8	1768	2	T13349	parallel sister ch
3	62	19.7	806	2	S22765	heterogeneous ribo
4	61.5	19.5	250	2	T23644	hypothetical prote
5	61.5	19.5	470	2	AH3594	virulence protein
6	61	19.4	1028	2	AS6038	DNA-binding protei
7	61	19.4	1213	2	SI6356	ovo protein - frui
8	60.5	19.2	379	2	T29518	hypothetical prote
9	60.5	19.2	713	2	B84583	hypothetical prote
10	60	19.0	717	2	T22938	hypothetical prote
11	59	18.7	307	2	T40815	transcription init
12	59	18.7	430	1	A46216	transcription fact
13	59	18.7	512	2	JC4164	catalase [EC 1.11.
14	59	18.7	532	2	T42369	catalase [EC 1.11.
15	59	18.7	565	2	T10696	legumin-like prote
16	59	18.7	626	2	T09345	hypothetical prote
17	59	18.7	2342	2	T13412	hypothetical prote
18	58.5	18.6	246	2	T12585	Dc3 promoter-bindi
19	58.5	18.6	365	2	T43286	cet-1 protein - Ca
20	58.5	18.6	458	2	S24457	hypothetical prote
21	58.5	18.6	535	2	S74703	hypothetical prote
22	58.5	18.6	750	2	D80802	protein T05A8.4 (i
23	58.5	18.6	769	2	T16245	hypothetical prote
24	58	18.4	255	2	T44991	oxidoreductase [m
25	58	18.4	351	2	B89781	conserved hypothet
26	58	18.4	504	2	T10698	legumin-like prote
27	58	18.4	508	2	B81594	hypothetical prote
28	58	18.4	508	2	B86549	hypothetical prote
29	58	18.4	508	2	C72074	hypothetical prote

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Qy 1 ENKLRSPVNLPELRRQRSGEVENNSD-NSGRYQGLEHHRGSEASPALPG 48
      :|||:|||||:
Db 54 EEKAQSNVYVPPHLRRQKENEERKFSALKASRSQSDTGTGSEEGASG 102

RESULT 5
AH3594
virulence protein [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 28-0
C:Accession: AH3594
R:DelVecchio, V.G.; Kapstral, V.; Redkar, R.J.; Patra, G.; Mujter, C.;
  Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Neil,
  Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen
A:Reference number: AD3252; PMID:11756688
A:Accession: AH3594
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-470 <KUR>
A:Cross-references: GB:AE080918; PIDN:AAL53923.1; PID:g17984866; GSI
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEII0681
A:Map position: II
C:Superfamily: type IV secretory pathway, VirJ component

Query Match 19.5%; Score 61.5; DB 2; Length 470;
Best Local Similarity 32.8%; Pred. No. 17;
Matches 22; Conservative 8; Mismatches 26; Indels 11;

Qy 6 SPVNLPELRRQRSGEVENNSDNGRVQ-----GLEHRGSEASPA--LP 48
      :|||:|||||:
Db 216 SPVNNPVEARKNIATLQTAPDFESARKMAVDNVVAMADQAKNEALPIIDL 102

Qy 55 QVALVYS 61
      :|||:
Db 276 MVAVFYS 282

RESULT 6
A56038
DNA-binding protein ovo - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-0
C:Accession: A56038
R:Garfinkel, M.D.; Wang, J.; Liang, Y.; Mahowald, A.P.
  Mol. Cell. Biol. 14, 6809-6818, 1994
A:Title: Multiple products from the shavenbaby-ovo gene region of D
A:Reference number: A56038; MUID:95021209; PMID:7935398
A:Accession: A56038
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1028 <GAR>
A:Cross-references: UNIPROT:P51521; GB:U11393; NID:g520526; PIDN:AA
C:Genetics:
A:Gene: ovo
A:Cross-references: FlyBase:FBgn0003028

Query Match 19.4%; Score 61; DB 2; Length 1028;
Best Local Similarity 36.1%; Pred. No. 47;
Matches 13; Conservative 6; Mismatches 17; Indels 0;

Qy 10 LPPELRRQRSGEVENNSDNGRYQGLEHHRGSEASPA 45
      :|||:|||||:
Db 21 LPPEYSLKSGQQQTASNTQSPFGANHSHFNANPA 56

RESULT 7
SI6356
ovo protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster

```

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S16356
R:Mevel-Ninio, M.; Terracol, R.; Kafatos, F.C.
EMBO J. 10, 2259-2266, 1991
A>Title: The ovo gene of Drosophila encodes a zinc finger protein required for female germline development
A:Reference number: S16356; MUID:91293102; PMID:1712294
A:Accession: S16356
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-1213 <MEV>
A:Cross-references: UNIPROT:Q8T8L9; EMBL:X59772
C:Genetics:
A:Gene: FlyBase:ovo
A:Cross-references: FlyBase:FBgn0003028
A:Introns: 931/3; 1152/3

Query Match 19.4%; Score 61; DB 2; Length 1213;
Best Local Similarity 36.1%; Pred. No. 57;
Matches 13; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 10 LPPELRQRSGEVENNSDNGRYQGLEHGRGSEASPA 45
DB 384 LPFFVESLKSQGSTASNTGQSPGANHSFNANPA 419

RESULT 8
T29518
hypothetical protein T25F10.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29518
R:Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid T25F10.
A:Reference number: Z20634
A:Accession: T29518
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-379 <PAU>
A:Cross-references: UNIPROT:O02424; EMBL:U64856; PIDN:AA04986.1; GSPDB:GN00023; CESP:T25F10
A:Experimental source: strain Bristol N2; clone T25F10
C:Genetics:
A:Gene: CESP:T25F10.2
A:Map position: 5
A:Introns: 96/3; 129/3; 153/3; 250/3; 286/1; 324/3; 362/2
C:Superfamily: inhibin

Query Match 19.2%; Score 60.5; DB 2; Length 379;
Best Local Similarity 34.1%; Pred. No. 18;
Matches 14; Conservative 9; Mismatches 17; Indels 1; Gaps 1;

QY 6 SPVNLPPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPAL 46
DB 224 SDSLSEPSVVRKRSQAT-GNSERKVRKGRKHNTAESNL 263

RESULT 9
B84583
hypothetical protein At2g19950 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84583
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: B84583
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-713 <STO>
A:Cross-references: UNIPROT:Q8S8N9; GB:AE002093; NID:g6598515; PIDN:AAF18622.1; GSPDB:GN

C:Genetics:
A:Gene: At2g19950
A:Map position: 2

Query Match 19.2%; Score 60.5; DB 2; Length 713;
Best Local Similarity 35.5%; Pred. No. 36;
Matches 22; Conservative 9; Mismatches 24; Indels 7; Gaps 2;

QY 1 ENKLSPVNLPPEL-RRQRSGEVENNSDNGRYQGLEHGRGSEASPALGKLKLSA 53
DB 385 EKLSSLQALRELAETERRAEERSAHHNATGAAMERERELEHRAVDASTALVRIQRTA 444

QY 54 DQ 55
DB 445 DE 446

RESULT 10
T22938
hypothetical protein F58G11.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22938
R:Pericy, C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19640
A:Accession: T22938
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-717 <WIL>
A:Cross-references: UNIPROT:Q9XVM1; EMBL:Z81094; PIDN:CAB03149.1; GSPDB:GN00023; CESP:F58G11
A:Experimental source: clone F58G11
C:Genetics:
A:Gene: CESP:F58G11.5
A:Map position: 5
A:Introns: 41/1; 76/1; 122/3; 169/3; 220/2; 338/1; 429/3; 471/2; 632/2; 669/3

Query Match 19.0%; Score 60; DB 2; Length 717;
Best Local Similarity 43.6%; Pred. No. 42;
Matches 17; Conservative 1; Mismatches 15; Indels 6; Gaps 1;

QY 5 RSPVNLPPELRRQRSGEVENNSDNGRYQGLEHGRGSEAS 43
DB 574 RSPSRSPSPRRQRSGEVENNSDNGRYQGLEHGRGSEAS 606

RESULT 11
T40615
transcription initiation factor iif, beta subunit - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40615
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, December 1998
A:Reference number: Z21941
A:Accession: T40615
A>Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-307 <LYN>
A:Cross-references: UNIPROT:O94424; EMBL:AL034563; PIDN:CAA22523.1; GSPDB:GN00067; SPDB: B84583
A:Experimental source: strain 972h-; cosmid c660
C:Genetics:
A:Gene: SPDB:SPBC660.03C
A:Map position: 2
A:Introns: 175/3; 223/3
C:Keywords: transcription initiation

Query Match 18.7%; Score 59; DB 2; Length 307;
Best Local Similarity 30.2%; Pred. No. 21;
Matches 13; Conservative 8; Mismatches 14; Indels 8; Gaps 1;

QY 13 ELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALGKLKLSADQ 55

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Db 262 ELRNQASQSESS-----IDHTGKNTSPDNPGTNAERDE 296

RESULT 12
A46216
transcription factor Skn-1, splice form a - rat
N/Alternate names: Skn-1a
C/Species: Rattus norvegicus (Norway rat)
C/Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 05-Dec-1997
C/Accession: A46216
R/Andersen, B.; Schonemann, M.D.; Flynn, S.E.; Pearce II, R.V.; Singh, H.; Rosenfeld, M.
Science 260, 78-82, 1993
A/Title: Skn-1a and Skn-1i: two functionally distinct Oct-2-related factors expressed in
transcription factor Skn-1, splice form a - rat
A/Reference number: A46216; MUID:93219836; PMID:7682011
A/Accession: A46216
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-430 <AND>
A/Cross-references: GB:L23862; NID:g393220
A/Note: sequence extracted from NCB1 backbone (NCBIP:128572)
C/Superfamily: transcription factor Oct-2, homeobox homology; POU domain homology
C/Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
F;183-250/Domain: POU domain homology <POU>
F;275-331/Domain: homeobox homology <HOX>

Query Match 18.7%; Score 59; DB 1; Length 430;
Best Local Similarity 24.1%; Pred. No. 31;
Matches 20; Conservative 11; Mismatches 20; Indels 32; Gaps 3;

Qy 8 VNLPEEL-----RRQSGEVENNSDNG-----RYQGLEHR 38
Db 2 VNLPEELSEIKMGVADSTDRSTFGQVSGNDRGLDFNRQIKTDGLGTLHESLSHR 61
Qy 39 G---SEASPALGLKLSADQVAL 58
Db 62 PCHLTEGFTWMPGNQSGDMASL 84

RESULT 13
JC4164
Catalase (EC 1.11.1.6) precursor - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 27-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C/Accession: JC4164; PC4041; T41598
R/Nakagawa, C.W.; Mutoh, N.; Hayaishi, Y.
J. Biochem. 118, 109-116, 1995
A/Title: transcriptional regulation of catalase gene in the fission yeast Schizosacchar
A/Reference number: JC4164; MUID:96015157; PMID:8537298
A/Accession: JC4164
A/Molecule type: DNA
A/Residues: 1-512 <LNK>
A/Cross-references: UNIPROT:P55306; GB:D55675; NID:g1905773; PIDN:BA009526.1; PID:g87197
A/Accession: PC4041
A/Molecule type: protein
A/Residues: 277-286; 421-431 <NA2>
R/Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Boche, G.; Pohl, T.
submitted to the EMBL Data Library, October 1998
A/Reference number: 222003
A/Accession: T41598
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-512 <LYN>
A/Cross-references: EMBL:AL031825; PIDN:CAA21232.1; GSPDB:GN00068; SPDB:SPCC757.07C
A/Experimental source: strain 972h-; cosmid c757
C/Comment: This enzyme is induced 8-fold in response to low concentrations of hydrogen H
C/Genetics:
A/Gene: catal; SPDB:SPCC757.07C
A/Map position: 3
C/Superfamily: catalase
C/Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-512/Product: catalase #status predicted <MAR>
F;60,99,133/Active site: His, Ser, Asn #status predicted
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Job time : 24.7042 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 19, 2004, 23:32:13 ; Search time 221.803 Seconds
(without alignments)
160.833 Million cell updates/sec

Title: US-10-068-725-4_COPY_105_166

Perfect score: 315

Sequence: 1 ENKLRSPVNLPELRQRSG.....SPALPGLKLSADQVALVYST 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	315	100.0	247	Q726F5	Q726F5 homo sapien
2	315	100.0	293	T13X_HUMAN	O14836 homo sapien
3	141.5	44.9	249	T13X_MOUSE	Q9et35 mus musculus
4	140	44.4	156	Q9N146	Q9N146 macaca mula
5	84.5	26.8	702	Q9VH96	Q9VH96 drosophila
6	66	21.0	480	Q7Y118	Q7Y118 strongyloce
7	66	21.0	480	Q9GUY6	Q9GUY6 hemientrot
8	66	21.0	497	Q942X2	Q942X2 oryza sativ
9	66	21.0	509	Q98KE4	Q98KE4 rhizobium l
10	66	21.0	546	Q7VBZ9	Q7VBZ9 prochloroco
11	66	21.0	554	Q9JHT9	Q9Jht9 mus musculu
12	66	21.0	620	Q923H2	Q923h2 mus musculu
13	66	21.0	710	Q8CHT1	Q8cht1 mus musculu
14	65.5	20.8	677	Q8TEJ7	Q8tej7 homo sapien
15	65	20.6	835	Q8KRE4	Q8kre4 agrobacteri
16	64.5	20.5	87	Q8AY96	Q8ay96 ictalurus p
17	64.5	20.5	358	Q96BE7	Q96be7 homo sapien
18	64	20.3	433	Q7XK69	Q7xk69 oryza sativ
19	63.5	20.2	800	Q6BJB7	Q6bjb7 debaryomyce
20	63.5	20.2	1665	Q6FIZ5	Q6fiz5 candida gla
21	63	20.0	3374	Q8JIZ3	Q8jiz3 montana myo
22	62.5	19.8	315	Q73U36	Q73u36 mycobacteri
23	62.5	19.8	315	A806082	A806082 mycobacte
24	62.5	19.8	1092	Q7KVZ8	Q7kvz8 drosophila
25	62.5	19.8	1092	AAF45735	AAF45735 drosophil
26	62.5	19.8	1108	Q8MR12	Q8mr12 drosophila
27	62.5	19.8	1741	O46095	O46095 drosophila
28	62.5	19.8	1741	Q9W517	Q9w517 drosophila
29	62.5	19.8	1768	Q24153	Q24153 drosophila
30	62.5	19.8	6858	Q7QUW1	Q7quw1 giardia lam
31	62	19.7	824	ROU_HUMAN	Q00839 homo sapien

RESULT 1

Q726F5
ID Q726F5 PRELIMINARY; PRT; 247 AA.
AC Q726F5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane activator and CAML interactor.
GN Name=TNFRSF13B;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY302137; AAP57629.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
KW Transmembrane.
SQ SEQUENCE 247 AA; 26664 MW; 850E1F4C2578E8E6 CRC64;

Query Match 100.0%; Score 315; DB 2; Length 247;

Best Local Similarity 100.0%; Pred. No. 7.7e-29;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPELRQRSGEVNNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 60

Db 59 ENKLRSPVNLPELRQRSGEVNNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 118

QY 61 ST 62

Db 119 ST 120

RESULT 2

T13X_HUMAN

ID T13X_HUMAN STANDARD; PRT; 293 AA.

AC O14836;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane

DE activator and CAML interactor).

GN Name=TNFRSF13B; Synonyms=TACI;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=B-cell;

RX MEDLINE=97458245; PubMed=9311921;

RA von Buelow G.-U., Bram R.J.;

RT "NF-AT activation induced by a CAML-interacting member of the tumor
RT necrosis factor receptor superfamily";
RL Science 278:138-141(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION.
RX MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200;
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dinko D., Lapleur D.,
RA Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
RA Olsen H.S., Kanakara P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RT high affinity receptor for TNF family members APRIL and BLYS";
RL J. Biol. Chem. 275:35478-35485(2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stollina M.,
RA Boyle W.J., Sarosi I., Heu H., Senaldi G., Theill L.E.;
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity";
RL Nat. Immunol. 1:252-256(2000).
RN [5]
RP INTERACTIONS WITH TRAF2 AND TRAF5.
RX MEDLINE=20341628; PubMed=10880535;
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA Theill L.E., Colombero A., Solovjev I., Lee F., McCabe S., Elliott R.,
RA Miner K., Hawkins N., Guo J., Stollina M., Yu G., Wang J., Delaney J.,
RA Meng S.Y., Boyle W.J., Hsu H.;
RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT factor family member involved in B cell regulation";
RL J. Exp. Med. 192:137-143(2000).
CC -I- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity.
CC -I- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAML with its C-terminus.
CC -I- SUBCELLULAR LOCATION: Type III membrane protein.
CC -I- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
CC intestine and peripheral blood leukocytes. Expressed in resting B-
CC cells and activated T-cells, but not in resting T-cells.
CC -I- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC -I- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
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CC -----
CC EMBL; AF023614; AAC51790.1; -;
CC EMBL; BC028072; AAH28072.1; -;
CC HSSP; Q9Y275; IQOD.
CC Genew; HGNC:18153; TNFRSF13B.
CC MIM; 604907; -;
CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.
CC DR GO; GO:0004872; Fireceptor activity; TAS.
CC DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
CC DR InterPro; IPR001369; TNFR_C6.
CC DR PROSITE; PS00652; TNFR_NGFR_1; 1.
CC DR PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
CC KW Glycoprotein; Immune response; Receptor; Repeat; Signal-anchor;
CC Transmembrane.
CC FT DOMAIN 1 165 Extracellular (Potential).
CC FT TRANSMEM 166 186 Signal-anchor for type III membrane
CC FT DOMAIN 187 293 Cytoplasmic (Potential).
CC FT REPEAT 33 67 TNFR-Cys 1.
CC FT REPEAT 70 104 TNFR-Cys 2.
CC FT DISULFID 34 47 By similarity.
CC FT DISULFID 50 62 By similarity.
CC FT DISULFID 54 66 By similarity.
CC FT DISULFID 71 86 By similarity.
CC FT DISULFID 89 100 By similarity.
CC FT DISULFID 93 104 By similarity.
CC FT DISULFID 128 128 N-linked (GlcNAc. .) (Potential).
CC FT CONFLICT 251 251 P -> L (in Ref. 2).
CC SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;
Query Match 100.0%; Score 315; DB 1; Length 293;
Best Local Similarity 100.0%; Pred. No. 9.4e-29;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ENKLRSFVNLPPELRRQRSGEVNNSDNGRYGLEHRSSEASPALPGLKLSADQVALVY 60
DB 105 ENKLRSFVNLPPELRRQRSGEVNNSDNGRYGLEHRSSEASPALPGLKLSADQVALVY 164
QY 61 ST 62
DB 165 ST 166
RESULT 3
T13X MOUSE
ID T13X MOUSE STANDARD; PRT; 249 AA.
AC Q9ET35; Q9DBZ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
GN Name=tnfrsf13b; Synonyms=Taci;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=21177254; PubMed=10881172; DOI=10.1038/76889;
RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
RT "Identification of a receptor for BLYS demonstrates a crucial role in
RT humoral immunity";
RL Nat. Immunol. 1:37-41(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmel S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlee G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RN [3]
RP FUNCTION.
RX MEDLINE=20341628; PubMed=1080535;
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA Theill L.E., Colombero A., Solovyev I., Lee P., McCabe S., Elliott R.,
RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
RA Meng S.-Y., Boyle W.J., Hsu H.,
RT "TAC1 is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT factor family member involved in B cell regulation."
RL J. Exp. Med. 192:137-143 (2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21322748; PubMed=11429548; DOI=10.1038/99782;
RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.,
RT "TAC1-ligand interactions are required for T cell activation and
RT collagen-induced arthritis in mice."
RL Nat. Immunol. 2:632-637 (2001).
CC -!- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity (By
CC similarity).
CC -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CARD10 with its C-terminus (By similarity).
CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF257673; BAB00081.1; -;
DR EMBL; AK004668; BAB23457.1; -;
DR MGD; MGI:1889411; Tnfrsf13b.
DR GO; GO:0005887; C:integral to plasma membrane; IDA.
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; IDA.
DR InterPro; IPR001368; TNFR_c6.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.

DR PROSITE; PS005050; TNFR_NGFR_2; FALSE_NEG.
KW Immune response; Receptor; Repeat; Signal-anchor; Transmembrane.
FT DOMAIN 1 128 Extracellular (Potential).
FT TRANSMEM 129 149 Signal-anchor for type III membrane
FT protein (Potential).
FT DOMAIN 150 249 Cytoplasmic (Potential).
FT REPEAT 5 38 TNFR-Cys 1.
FT REPEAT 42 76 TNFR-Cys 2.
FT DISULFID 6 19 By similarity.
FT DISULFID 22 34 By similarity.
FT DISULFID 26 38 By similarity.
FT DISULFID 43 58 By similarity.
FT DISULFID 61 72 By similarity.
FT DISULFID 65 76 By similarity.
FT CONFLICT 137 137 I -> F (in Ref. 2).
SQ SEQUENCE 249 AA; 26947 MW; CB2F2D61C2931D81 CRC64;

Query Match 44.9%; Score 141.5; DB 1; Length 249;
Best Local Similarity 53.2%; Pred. No. 2.4e-08;
Matches 33; Conservative 7; Mismatches 13; Indels 9; Gaps 2;

QY 1 ENKLSPVNLPPELRRQRSGVEVNSDNGRYQGLEHRSSEASPALPGLKLSADQVALVY 60
Db 77 EKRPSSQANLQPELGPQAGEVEVRSDNSGRHQSGHG-----PGURLSSDQLTL-Y 127
QY 61 ST 62
Db 128 CT 129

RESULT 4
Q9N146 PRELIMINARY; PRT; 156 AA.
AC Q9N146;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Transmembrane activator (Fragment).
GN Name=NF-AT;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI TaxID=9544;
RN [1] -;
RP SEQUENCE FROM N.A.
RA Arredondo J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF227558; AAF73400.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
KW Transmembrane.
FT NON_TER 1
SQ SEQUENCE 156 AA; 16170 MW; 8AD74E4D17D511D0 CRC64;

Query Match 44.4%; Score 140; DB 2; Length 156;
Best Local Similarity 96.6%; Pred. No. 2e-08;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 34 GLEHRSSEASPALPGLKLSADQVALVYST 62
Db 1 GLEHRSSEASPALPGLKLSADQVALVYST 29

RESULT 5
Q9VH96 PRELIMINARY; PRT; 702 AA.
AC Q9VH96;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG8358-PA (GH26575p).
GN ORFNames=CG8358;
OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20196006; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anatolides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadutein E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin C.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster K., Gabrielson A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky T.C., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mentrulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RN Science 287:2185-2195(2000).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence.";
RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a Genomics perspective.";
RN Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Mira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.R., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RN SEQUENCE FROM N.A.
RP FLYBASE;
RG Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RN SEQUENCE FROM N.A.
RG FLYBASE;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RN SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; AB003683; AAF54423.1; -;
DR ENBL; AY069219; AAL39364.1; -;
DR FLYBASE; FBGN0037727; CG8358.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0008237; F-metalloprotease activity; IEA.
DR GO; GO:0004245; F-proteolysis activity; IEA.
DR GO; GO:0006508; P-proteolysis and peptidolysis; IEA.
DR InterPro; IPR000718; Peptidase M13.
DR InterPro; IPR008753; Peptidase M13 N.
DR InterPro; IPR006025; Pest M_Zn_BS.
DR Pfam; PF01431; Peptidase_M13; 1.
DR Pfam; PF05649; Peptidase_M13_N; 1.
DR PRINTS; PR00786; NEPRILYSIN.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
KW Hydroxylase; Metalloprotease; Protease; Zinc.
SQ SEQUENCE 702 AA; 80825 MW; 4F4CA1A39F1FOBB6 CRC64;
Query Match 26.8%; Score 84.5; DB 2; Length 702;
Best Local Similarity 40.0%; Pred. No. 0.44;
Matches 24; Conservative 9; Mismatches 12; Indels 15; Gaps 3
Qy 12 PELRRQRSEV---ENNSDNG-----RYQLEHFGSE-ASPALGKLKLSADOV 56
Db 578 PEISRRVNGKTTLDENIADNSGLRQALFYRSHRQQLLEHFGQERISDAMPGDLTPQQL 637
RESULT 6
Q7Y718 PRELIMINARY; PRT; 480 AA.
ID Q7Y718
AC Q7Y718
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lim homeodomain transcription factor 1.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinozoa; Echinacea; Echinoida; Strongylocentrotidae;
OX NCBI_TaxID=7668;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Oral ectoderm;
RA Oliveri P., Davidson E.H.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 2 LIM zinc-binding domains.
DR ENBL; AY339649; AAQ01662.1; -;
DR GO; GO:0005634; C-nucleus; IEA.
DR GO; GO:0003700; F-transcription factor activity; IEA.
DR GO; GO:0008270; F-zinc ion binding; IEA.

DR GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR001781; LIM.
 DR InterPro: IPR007107; LIM homeo.
 DR Pfam: PF00046; Homeobox; 1.
 DR Pfam: PF00412; LIM; 2.
 DR ProDom: PD000010; Homeobox; 1.
 DR ProDom: PD000094; LIM; 2.
 DR SMART: SM00389; HOX; 1.
 DR SMART: SM00132; LIM; 2.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS00071; HOMEBOX_2; 1.
 DR PROSITE: PS00478; LIM_DOMAIN_1; 2.
 DR PROSITE: PS00023; LIM_DOMAIN_2; 2.
 KW DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
 Zinc.
 SQ SEQUENCE 480 AA; 53720 MW; DB884B7CA0F5A575 CRC64;
 Query Match 21.0%; Score 66; DB 2; Length 480;
 Best Local Similarity 30.4%; Pred. No. 43;
 Matches 14; Conservative 10; Mismatches 18; Indels 4; Gaps 1;
 QY 6 SPVNLPELRQRSGEV-----ENNSDNGRYOGLEHRSSEASPALP 47
 Db 181 TPATTPDDLDRVKDASIMNNNNNNNNNNHREAGLENRENTAGIP 226
 RESULT 7
 Q9GUY6 PRELIMINARY; PRT; 480 AA.
 ID Q9GUY6
 AC Q9GUY6
 DT 01-WAR-2001 (TREMBLrel. 16, Created)
 DT 01-WAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Transcription factor Hplim1.
 GN Name=Hplim1;
 OS Hemiteletrocus pulcherrimus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Echinozoa; Echinacea; Echinozoa; Strongylocentrotidae;
 OC Hemiteletrocus.
 OC NCBI_TaxID=7650;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99325976; PubMed=10400389;
 RA Kawasaki T., Mitsunaga-Nakatsubo K., Takeda K., Akasaka K.,
 RA Shinada H.;
 RT "Lim1 related homeobox gene (Hplim1) expressed in sea urchin
 embryos.";
 RT Dev. Growth Differ. 41:273-282(1999).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kawasaki T., Mitsunaga-Nakatsubo K., Takeda K., Akasaka K.,
 RA Shinada H.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
 DR EMBL: AB049118; BAB13725.1; -.
 DR HSP: P06601; 1FJL.
 DR GO: GO:0005634; Cnucleus; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR009057; Homeodomain_like.
 DR InterPro: IPR001781; LIM.
 DR InterPro: IPR007107; LIM homeo.
 DR Pfam: PF00046; Homeobox; 1.
 DR Pfam: PF00412; LIM; 2.
 DR PRINTS: PR00024; HOMEBOX.
 DR SMART: SM00389; HOX; 1.
 DR SMART: SM00132; LIM; 2.
 DR PROSITE: PS00027; HOMEBOX_1; 1.
 DR PROSITE: PS00071; HOMEBOX_2; 1.

DR PROSITE: PS00478; LIM_DOMAIN_1; 2.
 DR PROSITE: PS00023; LIM_DOMAIN_2; 2.
 KW DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
 Zinc.
 SQ SEQUENCE 480 AA; 53636 MW; EDCBCCBEC841A5D6 CRC64;
 Query Match 21.0%; Score 66; DB 2; Length 480;
 Best Local Similarity 30.4%; Pred. No. 43;
 Matches 14; Conservative 10; Mismatches 18; Indels 4; Gaps 1;
 QY 6 SPVNLPELRQRSGEV-----ENNSDNGRYOGLEHRSSEASPALP 47
 Db 181 TPATTPDDLDRVKDASIMNNNNNNNNNNHREAGLENRENTAGIP 226
 RESULT 8
 Q942X2 PRELIMINARY; PRT; 497 AA.
 ID Q942X2
 AC Q942X2
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Putative serine/threonine kinase PBS1 protein.
 GN Name=P0492609.25;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arica K., Hamada M., Harada C.,
 RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
 RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 RA Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1.";
 RL Nature 420:312-316(2002).
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL: AP003266; BAB64203.1; -.
 DR Gramene; Q942X2; -.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0006468; F:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR011009; Kinase like.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR008271; Ser thr_pkin_AS.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot kinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 497 AA; 54925 MW; 6DB0C1FAPDE0213E CRC64;
 Query Match 21.0%; Score 66; DB 2; Length 497;
 Best Local Similarity 35.9%; Pred. No. 44;
 Matches 23; Conservative 11; Mismatches 20; Indels 10; Gaps 4;
 QY 4 LRSPVNLPELRQR--RSGEV---NNSDNGRYOGLEH---RGSE-ASPALPGKLSA 53
 Db 401 VRSPNHHSFDLRREARSRAEVSTSGDSGRSGRLDLDMTGSGSPAQTKRKRET 460
 QY 54 DQVA 57

RC	STRAIN-SARG / COMP 1375 / SS120;
RX	MEDLINE=22810154; PubMed=12917486;
RA	Dufrene A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
RA	Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
RA	Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,
RA	Scanlan D.J., Tandeau de Marsac N., Weisenbach J., Wincker P.,
RA	Wolf Y.I., Hesse W.R.;
RT	"Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
RT	a nearly minimal oxyphototrophic genome."
RL	Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
DR	EMBL; AE017163; AAP99987.1; --
DR	GO; GO:0008686; F:3.4 dihydroxy-2-butanone-4-phosphate syntha. . . ; IEA.
DR	GO; GO:0003935; F:GTP cyclohydrolase II activity; IEA.
DR	GO; GO:0009231; P:vitamin B2 biosynthesis; IEA.
DR	InterPro; IPRO00422; DHBP synthase.
DR	InterPro; IPRO00926; GTP cyclohydroII.
DR	Pfam; PF00926; DHBP synthase; 1.
DR	Pfam; PF00925; GTP Cyclohydro2; 1.
DR	ProDom; PD003034; DHBP synthase; 1.
DR	TIGRFAMs; TIGR00505; ribA; 1.
DR	TIGRFAMs; TIGR00506; ribS; 1.
KW	Complete proteome.
SW	SEQUENCE 546 AA; 60348 MW; 05453CB83073B5FE CRC64;
Query Match	21.0%; Score 66; DB 2; Length 546;
Best Local Similarity	27.9%; Pred. No. 50;
Matches 17; Conservative	12; Mismatches 24; Indels 8; Gaps 1;
Qy	5 RSPVNIUP-----ELRRQRSGEVENNDSNGRYQGLEHGRGSASPALPKGLKSADQV 56
Db	382 REPLVNPTDYNANYLAIRKTLGHYIGNDDSDGKYVIYWGKIVSSNMLSAYKNKAQEI 441
Qy	57 A 57
Db	442 A 442
RESULT 11	
Q9JHT9	PRELIMINARY; PRT; 554 AA.
ID	OSJHT9 PRELIMINARY; PRT; 554 AA.
AC	Q9JHT9;
DT	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Guanine nucleotide exchange factor.
GN	Name=Ngef; Synonyms=gef;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;	
[1]	SEQUENCE FROM N.A.
RP	TISSUE=Brain;
RC	MEDLINE=20241931; PubMed=10777665;
RX	Rodrigues N.R., Theodosiou A.M., Nesbit M.A., Campbell L.,
RA	Tandil A.T., Saranath D., Davies K.E.;
RT	"Characterization of Ngef, a novel member of the DbI family of genes
RT	expressed predominantly in the caudate nucleus.";
RL	Genomics 65:53-61(2000).
DR	EMBL; AJ238898; CAC00698.1; --
DR	HSSP; O08839; lBB9.
DR	MGD; MG1:1858414; Ngef.
DR	GO; GO:008151; P:cell growth and/or maintenance; IDA.
DR	InterPro; IPR001849; PH.
DR	InterPro; IPR011036; PH related.
DR	InterPro; IPR000219; RhGEF.
DR	InterPro; IPR001452; SH3.
DR	Pfam; PF00169; PH; 1.
DR	Pfam; PF00621; RhGEF; 1.
DR	Pfam; PF00018; SH3_1; 1.
DR	ProDom; PD000066; SH3; 1.
DR	SMART; SM00233; PH; 1.
DR	SMART; SM00125; RhGEF; 1.

DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50010; DH 2; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS50002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 554 AA; 64837 MW; 5F7A8FAFBFF5914 CRC64;
Query Match 21.0%; Score 66; DB 2; Length 554;
Best Local Similarity 32.1%; Pred. No. 51;
Matches 17; Conservative 8; Mismatches 22; Indels 6; Gaps 1;
QY 13 ELRRQSGEVENNSDNS-----GRYQGLEHRSSEASPALGLKLSADQVALV 59
Db 34 ETRQQDAIQNSDGSQVGDAGEEEEEEEELASPPERRALPOICLL 86
RESULT 12
Q923H2 PRELIMINARY; PRT; 620 AA.
AC Q923H2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ephexin.
GN Name=Ngef;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=21234975; PubMed=11336673;
RA Shamah S.M., Lin M.Z., Goldberg J.L., Estrach S., Sahlin M., Hu L.,
BA Bazalakova M., Neve R., Corfas G., Debant A., Greenberg M.E.;
RT "Epha receptors regulate growth cone dynamics through the novel
guanine nucleotide exchange factor ephexin.";
RL Cell 105:233-244(2001).
DR EMBL; AY038025; AAK71494.1; -.
DR HSSP; O08839; 1BB9.
DR MGD; MGI:1858414; Ngef.
DR GO; GO:0008151; P:cell growth and/or maintenance; IDA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000219; RhGGEF.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhGGEF; 1.
DR Pfam; PF00018; SH3; 1; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhGGEF; 1.
DR SMART; SM00326; SH3; 1; 1.
DR PROSITE; PS50010; DH 2; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS50002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 620 AA; 71445 MW; C2C3A9C156F78402 CRC64;
Query Match 21.0%; Score 66; DB 2; Length 620;
Best Local Similarity 32.1%; Pred. No. 58;
Matches 17; Conservative 8; Mismatches 22; Indels 6; Gaps 1;
QY 13 ELRRQSGEVENNSDNS-----GRYQGLEHRSSEASPALGLKLSADQVALV 59
Db 100 ETRQQDAIQNSDGSQVGDAGEEEEEEEELASPPERRALPOICLL 152
RESULT 13
Q8CHT1 PRELIMINARY; PRT; 710 AA.
ID Q8CHT1
AC Q8CHT1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ngef protein.
GN Name=Ngef;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC039279; AAH39279.1; -.
DR HSSP; O08839; 1BB9.
DR MGD; MGI:1858414; Ngef.
DR GO; GO:0008151; P:cell growth and/or maintenance; IDA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR000219; RhGGEF.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhGGEF; 1.
DR Pfam; PF00018; SH3; 1; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhGGEF; 1.
DR SMART; SM00326; SH3; 1; 1.
DR PROSITE; PS50010; DH 2; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS50002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 710 AA; 82198 MW; F255DE351E02A586 CRC64;
Query Match 21.0%; Score 66; DB 2; Length 710;
Best Local Similarity 32.1%; Pred. No. 68;
Matches 17; Conservative 8; Mismatches 22; Indels 6; Gaps 1;
QY 13 ELRRQSGEVENNSDNS-----GRYQGLEHRSSEASPALGLKLSADQVALV 59
Db 190 ETRQQDAIQNSDGSQVGDAGEEEEEEEELASPPERRALPOICLL 242
RESULT 14
Q8TEJ7 PRELIMINARY; PRT; 677 AA.
ID Q8TEJ7
AC Q8TEJ7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

